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| (54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE (57) Abstract Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides. | | |

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COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

TECHNICAL FIELD

The present invention relates generally to compositions and methods for the treatment of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein and to DNA molecules encoding such polypeptides. Such polypeptides may be used in vaccines and pharmaceutical compositions for treatment of prostate cancer.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved vaccines and treatment methods for prostate cancer.

SUMMARY OF THE INVENTION

The present invention provides compounds and methods for immunotherapy of prostate cancer. In one aspect, polypeptides are provided comprising at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants thereof.

In related aspects, DNA molecules encoding the above polypeptides are provided. In specific embodiments, such DNA molecules include sequences provided in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224. The present invention further provides expression vectors comprising the above DNA molecules and host cells transformed or transfected with such expression vectors. In preferred embodiments, the host cells are selected from the group consisting of *E. coli*, yeast and mammalian cells.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known prostate antigen.

The present invention also provides pharmaceutical compositions comprising one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier, together with vaccines comprising one or more of such polypeptide or DNA molecules in combination with a non-specific immune response enhancer.

In related aspects, pharmaceutical compositions for the treatment of prostate cancer comprising one or more polypeptides and a physiologically acceptable carrier are provided, wherein the polypeptide comprises an immunogenic portion of a prostate tumor protein or of a variant of said protein that differs only in conservative substitutions and/or modifications, the prostate tumor protein being encoded by a DNA molecule having a

sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants thereof. The invention also provides vaccines for the treatment of prostate cancer comprising such polypeptides in combination with a non-specific immune response enhancer, together with pharmaceutical compositions and vaccines comprising one or more DNA molecules having a sequence provided in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221. Pharmaceutical compositions and vaccines comprising one or more of the above fusion proteins are also provided.

In yet another aspect, methods are provided for inhibiting the development of prostate cancer in a patient, comprising administering an effective amount of at least one of the above pharmaceutical compositions and/or vaccines.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunotherapy of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant of such a protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-

65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 181, 188, 191, 193, 194, 198, 203, 204, and 207-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of

one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recite nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers

to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a

growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain preferred embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end

of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may generally be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the

immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or fusion proteins comprising one or more such polypeptides and/or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides (or fusion proteins or DNA molecules encoding such polypeptides) may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide or fusion protein is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (*e.g.*, polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the

use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (*i.e.*, untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary

depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATE™ system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

Polypeptides of the present invention may also, or alternatively, be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the

above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (i.e., sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (i.e., the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (*e.g., mice, rats, rabbits, sheep and goats*). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e., reactivity with the polypeptide of interest*). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

Example 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor

library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 μ g) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 μ l of H₂O, heat-denatured and mixed with 100 μ l (100 μ g) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 μ l) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 μ l H₂O to form the driver DNA.

To form the tracer DNA, 10 μ g prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 μ l H₂O. Tracer DNA was mixed with 15 μ l driver DNA and 20 μ l of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 μ l H₂O, mixed with 8 μ l driver DNA and 20 μ l of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into

BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was

performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are

provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS:

93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively. cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Example 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR
POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in

prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal

colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no

significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

Example 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Xu, Jiangchun
Dillin, Davin C.
- (ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER
AND METHODS FOR THEIR USE
- (iii) NUMBER OF SEQUENCES: 224
- (iv) CORRESPONDENCE ADDRESS:
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 - (C) CITY: Seattle
 - (D) STATE: WA
 - (E) COUNTRY: USA
 - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 23-FEB-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Maki, David J.
 - (B) REGISTRATION NUMBER: 31,392
 - (C) REFERENCE/DOCKET NUMBER: 210121.427C3
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 622-4900
 - (B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTCACAG | TATAACAGCT | CTTTATTTCT | GTGAGTTCTA | CTAGGAAATC | 60 |
| ATCAAATCTG | AGGGTTGTCT | GGAGGACTTC | AATACACCTC | CCCCCATAGT | GAATCAGCTT | 120 |
| CCAGGGGGTC | CAGTCCCTCT | CCTTACTTCA | TCCCATCCC | ATGCCAAAGG | AAGACCCTCC | 180 |
| CTCCTTGGCT | CACAGCCTTC | TCTAGGCTTC | CCAGTGCCTC | CAGGACAGAG | TGGGTTATGT | 240 |
| TTTCAGCTCC | ATCCTTGCTG | TGAGTGTCTG | GTGCGTTGTG | CCTCCAGCTT | CTGCTCAGTG | 300 |
| CTTCATGGAC | AGTGTCCAGC | ACATGTCACT | CTCCACTCTC | TCAGTGTGGA | TCCACTAGTT | 360 |
| CTAGAGCGGC | CGCCACCGCG | GTGGAGCTCC | AGCTTTTGTT | CCCTTTAGTG | AGGGTTAATT | 420 |

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GCGCGCTTGG | CGTAATCATG | GTCATAACTG | TTTCCTGTGT | GAAATTGTTA | TCCGCTCACA | 480 |
| ATTCCACACA | ACATACGAGC | CGGAAGCATA | AAGTGTAAG | CCTGGGGTGC | CTAATGAGTG | 540 |
| ANCTAACTCA | CATTAATTGC | GTTCGCTCA | CTGNCCGCTT | TCCAGTCNGG | AAAACTGTCTG | 600 |
| TGCCAGCTGC | ATTAATGAAT | CGGCCAACGC | NCGGGGAAAA | GCGGTTTGCG | TTTGGGGGC | 660 |
| TCTTCCGCTT | CTCGCTCACT | NANTCCTGCG | CTCGGTCNTT | CGGCTGCGGG | GAACGGTATC | 720 |
| ACTCCTCAAA | GGNGGTATTA | CGGTTATCCN | NAAATCNGGG | GATACCCNGG | AAAAAANTTT | 780 |
| AACAAAAGGG | CANCAAAGGG | CNGAAACGTA | AAAA | | | 814 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|-----|
| ACAGAAATGT | TGGATGGTGG | AGCACCTTTC | TATACGACTT | ACAGGACAGC | AGATGGGGAA | 60 |
| TTCATGGCTG | TTGAGCAAT | AGAACCCAG | TTCTACGAGC | TGCTGATCAA | AGGACTTGGA | 120 |
| CTAAAGTCTG | ATGAACCTCC | CAATCAGATG | AGCATGGATG | ATTGGCCAGA | AATGAAGAAG | 180 |
| AAGTTTGCG | ATGTATTTGC | AAAGAAGACG | AAGGCAGAGT | GGTGTCAAAT | CTTTGACGGC | 240 |
| ACAGATGCCT | GTGTGACTCC | GGTTCTGACT | TTTGAGGAGG | TTGTTTCATCA | TGATCACAAC | 300 |
| AAGGAACGGG | GCTCGTTTAT | CACCACTGAG | GAGCAGGACG | TGAGCCCCCG | CCCTGCACCT | 360 |
| CTGCTGTTAA | ACACCCACAGC | CATCCCTTCT | TTCAAAGGG | ATCCACTAGT | TCTAGAAGCG | 420 |
| GCCGCCACCG | CGGTGGAGCT | CCAGCTTTTG | TTCCCTTTAG | TGAGGGTTAA | TTGCGCGCTT | 480 |
| GGCGTAATCA | TGGTCATAGC | TGTTTCCTGT | GTGAAATTGT | TATCCGCTCA | CAATTCCCCC | 540 |
| AACATACGAG | CCGGAACATA | AAGTGTTAAG | CCTGGGGTGC | CTAATGANTG | AGCTAACTCN | 600 |
| CATTAATTGC | GTTCGCTCA | CTGCCGCTT | TCCAGTCGGG | AAAACTGTCG | TGCCACTGCN | 660 |
| TTANTGAATC | NGCCACCCCC | CGGAAAAGG | CGGTTGCNTT | TTGGGCCTCT | TCCGCTTTCC | 720 |
| TCGCTCATTG | ATCCTNGCNC | CCGGTCTTCG | GCTGCGNGA | ACGGTTCACT | CCTCAAAGGC | 780 |
| GGTNTNCCGG | TTATCCCCAA | ACNGGGGATA | CCNGA | | | 816 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CTTTTGAAAG | AAGGGATGGC | TGGGGTGTTT | AACAGCAGAG | GTGCAGGGCG | GGGGCTCAGC | 60 |
| TCCTGCTCCT | CACTGGTGAT | AAACGAGCCC | CGTTCCTTGT | TGTGATCATG | ATGAACAACC | 120 |
| TCCTCAAAAG | TCAGAACCGG | AGTCACACAG | GCATCTGTGC | CGTCAAAGAT | TTGACACCAC | 180 |
| TCTGCCTTCG | TCTTCCTTGC | AAATACATCT | GCAAACTTCT | TCTTCATTTC | TGGCCAATCA | 240 |
| TCCATGCTCA | TCTGATTGGG | AAGTTCATCA | GACTTTAGTC | CANNTCCTTT | GATCAGCAGC | 300 |
| TCGTAGAACT | GGGGTTCTAT | TGCTCCAACA | GCCATGAATT | CCCCATCTGC | TGTCCTGTAA | 360 |
| GTCGTATAGA | AAGGTGCTCC | ACCATCCAAC | ATGTTCTGTC | CTCGAGGGGG | GGCCCGGTAC | 420 |
| CCAATTTCGCC | CTATANTGAG | TCGTATTACG | CGCGCTCACT | GGCCGTCGTT | TTACAACGTC | 480 |
| GTGACTGGGA | AAACCCTGGG | CGTTACCAAC | TTAATCGCCT | TGCAGCACAT | CCCCCTTTCG | 540 |
| CCAGCTGGGC | GTAATANCGA | AAAGGCCCGC | ACCGATCGCC | CTTCCAACAG | TTGCGCACCT | 600 |
| GAATGGGNAA | ATGGGACCCC | CCTGTTACCG | CGCATTNAAC | CCCCGCNNGG | TTTNGTTGTT | 660 |
| ACCCCCACNT | NNACCGCTTA | CACTTTGCCA | GCGCCTTANC | GCCCGCTCCC | TTTCNCCTTT | 720 |
| CTTCCCTTCC | TTTCNCNCCN | CTTTCCTCCG | GGGTTTCCCC | CNTCAAACCC | CNA | 773 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| CCTCCTGAGT | CCTACTGACC | TGTGCTTTCT | GGTGTGGAGT | CCAGGGCTGC | TAGGAAAAGG | 60 |
| AATGGGCAGA | CACAGGTGTA | TGCCAATGTT | TCTGAAATGG | GTATAATTTC | GTCCCTCTCCT | 120 |
| TCGGAACACT | GGCTGTCTCT | GAAGACTTCT | CGCTCAGTTT | CAGTGAGGAC | ACACACAAAG | 180 |
| ACGTGGGTGA | CCATGTTGTT | TGTGGGGTGC | AGAGATGGGA | GGGTGGGGC | CCACCCTGGA | 240 |
| AGAGTGGACA | GTGACACAAG | GTGGACACTC | TCTACAGATC | ACTGAGGATA | AGCTGGAGCC | 300 |
| ACAATGCATG | AGGCACACAC | ACAGCAAGGA | TGACNCTGTA | AACATAGCCC | ACGCTGTCCT | 360 |
| GNGGGCACTG | GGAAGCCTAN | ATNAGGCCGT | GAGCANAAAG | AAGGGGAGGA | TCCACTAGTT | 420 |
| CTANAGCGGC | CGCCACCGCG | GTGGANCTCC | ANCTTTTGTT | CCCTTTAGTG | AGGGTTAATT | 480 |
| GCGCGCTTGG | CNTAATCATG | GTCATANCTN | TTTCCTGTGT | GAAATGTGTA | TCCGCTCACA | 540 |
| ATTCCACACA | ACATACGANC | CGGAAACATA | AANTGTAAAC | CTGGGGTGCC | TAATGANTGA | 600 |
| CTAACTCACA | TTAATTGCGT | TGCGCTCACT | GCCCGCTTTC | CAATCNGGAA | ACCTGTCTTG | 660 |
| CCNCTTG CAT | TNATGAATCN | GCCAACCCCC | GGGGAAAAGC | GTTTGCGTTT | TGGGCGCTCT | 720 |
| TCCGCTTCCT | CNCTCANTTA | NTCCCTNCNC | TCGGTCATTC | CGGCTGCNGC | AAACCGGTTC | 780 |
| ACCNCCTCCA | AAGGGGGTAT | TCCGGTTTCC | CCNAATCCGG | GGANANCC | | 828 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTACTGA | TAGATGGAAT | TTATTAAGCT | TTTCACATGT | GATAGCACAT | 60 |
| AGTTTTTAAT | GCATCCAAAG | TACTAACAAA | AACTCTAGCA | ATCAAGAATG | GCAGCATGTT | 120 |
| ATTTTATAAC | AATCAACACC | TGTGGCTTTT | AAAATTTGGT | TTTCATAAGA | TAATTTATAC | 180 |
| TGAAGTAAAT | CTAGCCATGC | TTTTAAAAAA | TGCTTTAGGT | CACTCCAAGC | TTGGCAGTTA | 240 |
| ACATTTGGCA | TAAACAATAA | TAAAACAATC | ACAATTTAAT | AAATAACAAA | TACAACATTG | 300 |
| TAGGCCATAA | TCATATACAG | TATAAGGAAA | AGGTGGTAGT | GTTGAGTAAG | CAGTTATTAG | 360 |
| AATAGAATAC | CTTGGCCTCT | ATGCAAATAT | GTCTAGACAC | TTTGATTAC | TCAGCCCTGA | 420 |
| CATTCAGTTT | TCAAAGTAGG | AGACAGGTTC | TACAGTATCA | TTTTACAGTT | TCCAACACAT | 480 |
| TGAAAACAAG | TAGAAAATGA | TGAGTTGATT | TTTATTAATG | CATTACATCC | TCAAGAGTTA | 540 |
| TCACCAACCC | CTCAGTTATA | AAAAATTTTC | AAGTTATATT | AGTCATATAA | CTTGGTGTGC | 600 |
| TTATTTTAAA | TTAGTGCTAA | ATGGATTAA | TGAAGACAAC | AATGGTCCCC | TAATGTGATT | 660 |
| GATATTGGTC | ATTTTACCA | GCTTCTAAAT | CTNAACTTTC | AGGCTTTTGA | ACTGGAACAT | 720 |
| TGNATNACAG | TGTTCCANAG | TTNCAACCTA | CTGGAACATT | ACAGTGTGCT | TGATTCAAAA | 780 |
| TGTTATTTTG | TTAAAAATTA | AATTTTAACC | TGGTGGAAAA | ATAATTTGAA | ATNA | 834 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | AAGACCTCA | TCAATAGATG | GAGACATACA | GAAATAGTCA | 60 |
| AACCACATCT | ACAAAATGCC | AGTATCAGGC | GGCGGCTTCG | AAGCCAAAGT | GATGTTTGGG | 120 |
| TGTAAAGTGA | AATATTAGTT | GGCGGATGAA | GCAGATAGTG | AGGAAAGTTG | AGCCAATAAT | 180 |
| GACGTGAAGT | CCGTGGAAGC | CTGTGGCTAC | AAAAAATGTT | GAGCCGTAGA | TGCCGTCGGA | 240 |
| AATGGTGAAG | GGAGACTCGA | AGTACTCTGA | GGCTTGTAAG | AGGGTAAAT | AGAGACCCAG | 300 |
| TAAATTGTA | ATAAGCAGTG | CTTGAATTAT | TTGGTTTCGG | TTGTTTTCTA | TTAGACTATG | 360 |
| GTGAGCTCAG | GTGATTGATA | CTCCTGATGC | GAGTAATACG | GATGTGTTTA | GGAGTGGGAC | 420 |
| TTCTAGGGGA | TTTAGCGGGG | TGATGCCTGT | TGGGGGCCAG | TGCCCTCCTA | GTTGGGGGGT | 480 |
| AGGGGCTAGG | CTGGAGTGGT | AAAAGGCTCA | GAAAAATCCT | GCGAAGAAAA | AAACTTCTGA | 540 |
| GGTAATAAAT | AGGATTATCC | CGTATCGAAG | GCCTTTTGG | ACAGGTGGTG | TGTGGTGGCC | 600 |
| TTGGTATGTG | CTTCTCGTG | TTACATCGCG | CCATCATTGG | TATATGGTTA | GTGTGTTGGG | 660 |
| TTANTANGGC | CTANTATGAA | GAACCTTTGG | ANTGGAATTA | AATCAATNGC | TTGGCCGGAA | 720 |
| GTCATTANGA | NGGCTNAAAA | GGCCCTGTGA | NGGGTCTGGG | CTNGGTTTGA | CCCNACCCAT | 780 |
| GGAATNCNCC | CCCCGGACNA | NTGNATCCCT | ATTCTTAA | | | 818 |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TGGCTCTAGA | GGGGGTAGAG | GGGGTGCTAT | AGGGTAAATA | 60 |
| CGGGCCCTAT | TTCAAAGATT | TTTAGGGGAA | TTAATTCTAG | GACGATGGGT | ATGAAACTGT | 120 |
| GGTTTGCTCC | ACAGATTTCA | GAGCATTGAC | CGTAGTATAC | CCCCGGTCGT | GTAGCGGTGA | 180 |
| AAGTGGTTTG | GTTTAGACGT | CCGGGAATTG | CATCTGTTT | TAAGCCTAAT | GTGGGGACAG | 240 |
| CTCATGAGTG | CAAGACGTCT | TGTGATGTAA | TTATTATACN | AATGGGGGCT | TCAATCGGGA | 300 |
| GTACTACTCG | ATTGTCAACG | TCAAGGAGTC | GCAGGTCCGC | TGGTTCTAGG | AATAATGGGG | 360 |
| GAAGTATGTA | GGAATTGAAG | ATTAATCCGC | CGTAGTCGGT | GTTCTCCTAG | GTTCAATACC | 420 |
| ATTGGTGGCC | AATTGATTTG | ATGGTAAGGG | GAGGGATCGT | TGAACCTGTC | TGTTATGTAA | 480 |
| AGGATNCCTT | NGGGATGGGA | AGGCNATNAA | GGACTANGGA | TNAATGGCGG | GCANGATATT | 540 |
| TCAAACNGTC | TCTANTTCCT | GAAACGTCTG | AAATGTTAAT | AANAATTAA | TTTNGTTATT | 600 |
| GAATNTTNG | GAAAAGGGCT | TACAGGACTA | GAAACCAAAT | ANGAAAANTA | ATNNTAANGG | 660 |
| CNTTATCNTN | AAAGGTNATA | ACCNCTCCTA | TNATCCCACC | CAATNGNATT | CCCCACNCNN | 720 |
| ACNATTGGAT | NCCCCANTTC | CANAAANGGC | CNCCCCCGG | TGNANNCCNC | CTTTTGTTCC | 780 |
| CTTNANTGAN | GGTTATTNC | CCCTNGCNTT | ATCANCC | | | 817 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CATTTCCGGG | TTTACTTTCT | AAGGAAAGCC | GAGCGGAAGC | TGCTAACGTG | GGAATCGGTG | 60 |
| CATAAGGAGA | ACTTTCTGCT | GGCACGCGCT | AGGGACAAGC | GGGAGAGCGA | CTCCGAGCGT | 120 |

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| CTGAAGCGCA | CGTCCCAGAA | GGTGGACTTG | GCACTGAAAC | AGCTGGGACA | CATCCGCGAG | 180 |
| TACGAACAGC | GCCTGAAAGT | GCTGGAGCGG | GAGGTCCAGC | AGTGTAGCCG | CGTCCTGGGG | 240 |
| TGGGTGGCCG | ANGCCTGANC | CGCTCTGCCT | TGCTGCCCCC | ANGTGGGCCG | CCACCCCTG | 300 |
| ACCTGCCTGG | GTCCAAACAC | TGAGCCCTGC | TGGCGGACTT | CAAGGANAAC | CCCCACANGG | 360 |
| GGATTTTGCT | CCTANANTAA | GGCTCATCTG | GGCCTCGGCC | CCCCCACCTG | GTTGGCCTTG | 420 |
| TCTTTGANGT | GAGCCCCATG | TCCATCTGGG | CCACTGTCNG | GACCACCTTT | NGGGAGTGTT | 480 |
| CTCCTTACAA | CCACANNATG | CCCGGCTCCT | CCCGGAAACC | ANTCCCANCC | TGNGAAGGAT | 540 |
| CAAGNCCTGN | ATCCACTNNT | NCTANAACCG | GCCNCCNCCG | CNGTGGAAACC | CNCCTTNTGT | 600 |
| TCCTTTTCNT | TNAGGGTTAA | TNNCGCCTTG | GCCTTNCCAN | NGTCCTNCNC | NTTTTCCNNT | 660 |
| GTTNAAATTG | TTANGCNCCC | NCCNNTCCCN | CNNCNCNAN | CCCGACCCNN | ANNTTNNANN | 720 |
| NCCTGGGGGT | NCCNNCNGAT | TGACCCNNCC | NCCCTNTANT | TGCNTTNGGG | NNCINTGCCC | 780 |
| CTTTCCCTCT | NGGGANNCG | | | | | 799 |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACGCCTTGAT | CCTCCCAGGC | TGGGACTGGT | TCTGGGAGGA | GCCGGGCATG | CTGTGGTTTG | 60 |
| TAANGATGAC | ACTCCCAAAG | GTGGTCCTGA | CAGTGGCCCA | GATGGACATG | GGGCTCACCT | 120 |
| CAAGGACAAG | GCCACCAGGT | GCGGGGGCCG | AAGCCCACAT | GATCCTTACT | CTATGAGCAA | 180 |
| AATCCCCTGT | GGGGGCTTCT | CCTTGAAGTC | CGCCANCAGG | GCTCAGTCTT | TGGACCCANG | 240 |
| CAGGTCATGG | GGTTGTNGNC | CAACTGGGGG | CCNCAACGCA | AAANGGCNCA | GGGCCTCNGN | 300 |
| CACCCATCCC | ANGACGCGGC | TACACTNCTG | GACCTCCCNC | TCCACCACTT | TCATGCGCTG | 360 |
| TTCNTACCCG | CGNATNTGTC | CCANCTGTTT | CNGTGCCNAC | TCCANCTTCT | NGGACGTGCG | 420 |
| CTACATACGC | CCGGANTCNC | NCTCCCGCTT | TGTCCTTATC | CACGTNCCAN | CAACAAATTT | 480 |
| CNCCNTANTG | CACCNATTCC | CACNTTTNNC | AGNTTTCNC | NNCGNGCTTC | CTTNTAAAAG | 540 |
| GGTTGANCCC | CGGAAAATNC | CCCAAAGGGG | GGGGGCCNGG | TACCCAACTN | CCCCCTNATA | 600 |
| GCTGAANTCC | CCATNACCNN | GNCTCNATGG | ANCCNTCCNT | TTTAANNACN | TTCTNAACTT | 660 |
| GGGAANANCC | CTCGNCCNTN | CCCCNTTAA | TCCCNCCCTG | CNANGNNCNT | CCCCCNNTCC | 720 |
| NCCCNNTTNG | GCNTNTNANN | CNAAAAGGC | CCNNNANCAA | TCTCCTNNCN | CCTCANTTCG | 780 |
| CCANCCCTCG | AAATCGGCCN | C | | | | 801 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| CAGTCTATNT | GGCCAGTGTG | GCAGCTTTCC | CTGTGGCTGC | CGGTGCCACA | TGCCTGTCCC | 60 |
| ACAGTGTGGC | CGTGGTGACA | GCTTCAGCCG | CCCTCACC GG | GTTCACCTTC | TCAGCCCTGC | 120 |
| AGATCCTGCC | CTACACACTG | GCCTCCCTCT | ACCACCGGGA | GAAGCAGGTG | TTCTGCCCCA | 180 |
| AATACCGAGG | GGACACTGGA | GGTGCTAGCA | GTGAGGACAG | CCTGATGACC | AGCTTCCTGC | 240 |
| CAGGCCCTAA | GCCTGGAGCT | CCCTTCCCTA | ATGGACACGT | GGGTGCTGGA | GGCAGTGCC | 300 |
| TGCTCCCACC | TCCACCCGCG | CTCTGCGGGG | CCTCTGCCTG | TGATGTCTCC | GTACGTGTGG | 360 |
| TGGTGGGTGA | GCCCACCGAN | GCCAGGGTGG | TTCCGGGCGG | GGGCATCTGC | CTGGACCTCG | 420 |
| CCATCCTGGA | TAGTGCTTCC | TGCTGTCCCA | NGTGGCCCCA | TCCCTGTTTA | TGGGCTCCAT | 480 |
| TGTCCAGCTC | AGCCAGTCTG | TCACTGCCTA | TATGGTGTCT | GCCGCAGGCC | TGGGTCTGGT | 540 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCCATTACT | TTGCTACACA | GGTANTATTT | GACAAGAACG | ANTTGGCCAA | ATACTCAGCG | 600 |
| TTAAAAAATT | CCAGCAACAT | TGGGGGTGGA | AGGCCTGCCT | CACTGGGTCC | AACTCCCCGC | 660 |
| TCCTGTTAAC | CCCATGGGGC | TGCCGGCTTG | GCCGCAATT | TCTGTTGCTG | CCAAANTNAT | 720 |
| GTGGCTCTCT | GCTGCCACCT | GTGCTGGCT | GAAGTGCNTA | CNGCNCANCT | NGGGGGGTNG | 780 |
| GGNGTTCCC | | | | | | 789 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 772 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| CCCACCCTAC | CCAAATATTA | GACACCAACA | CAGAAAAGCT | AGCAATGGAT | TCCCTTCTAC | 60 |
| TTTGTTAAAT | AAATAAGTTA | AATATTTAAA | TGCCTGTGTC | TCTGTGATGG | CAACAGAAGG | 120 |
| ACCAACAGGC | CACATCCTGA | TAAAAGGTAA | GAGGGGGGTG | GATCAGCAAA | AAGACAGTGC | 180 |
| TGTGGGCTGA | GGGGACCTGG | TTCTTGTGTG | TTGCCCTCA | GGACTCTTCC | CCTACAAATA | 240 |
| ACTTTCATAT | GTTCAAATCC | CATGGAGGAG | TGTTTCATCC | TAGAAACTCC | CATGCAAGAG | 300 |
| CTACATTAAA | CGAAGCTGCA | GGTTAAGGGG | CTTANAGATG | GGAAACCAGG | TGACTGAGTT | 360 |
| TATTCAGCTC | CCAAAAACCC | TTCTCTAGGT | GTGTCTCAAC | TAGGAGGCTA | GCTGTTAACC | 420 |
| CTGAGCCTGG | GTAATCCACC | TGCAGAGTCC | CCGCATCCA | GTGCATGGAA | CCCTTCTGGC | 480 |
| CTCCCTGTAT | AAGTCCAGAC | TGAAACCCCC | TTGGAAGGNC | TCCAGTCAGG | CAGCCCTANA | 540 |
| AACTGGGGAA | AAAAGAAAAG | GACGCCCCAN | CCCCAGCTG | TGCANCTACG | CACCTCAACA | 600 |
| GCACAGGGTG | GCAGCAAAAA | AACCACTTTA | CTTTGGCACA | AACAAAAACT | NGGGGGGGCA | 660 |
| ACCCCGGCAC | CCCNANGGGG | GTTAACAGGA | ANCNGGGNAA | CNTGGAACCC | AATTNAGGCA | 720 |
| GGCCCNCCAC | CCCNAAATNTT | GCTGGGAAAT | TTTTCTCTCC | CTAAATTNTT | TC | 772 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GCCCCAATTC | CAGCTGCCAC | ACCACCCACG | GTGACTGCAT | TAGTTCGGAT | GTCATACAAA | 60 |
| AGCTGATTGA | AGCAACCCTC | TACTTTTTTG | TCGTGAGCCT | TTTGCTTGGT | GCAGGTTTCA | 120 |
| TGGCTGTGT | TGGTGACGTT | GTCAATTGCA | CAGAATGGGG | GAAAGGCAC | GTTCTCTTTG | 180 |
| AAGTANGGTG | AGTCTCAAA | ATCCGTATAG | TTGGTGAAGC | CACAGCACTT | GAGCCCTTTC | 240 |
| ATGGTGGTGT | TCCCACTTG | AGTGAAGTCT | TCCTGGGAAC | CATAATCTTT | CTTGATGGCA | 300 |
| GGCACTACCA | GCAACGTCAG | GGAAGTGCTC | AGCCATTGTG | GTGTACACCA | AGGCGACCAC | 360 |
| AGCAGCTGCN | ACCTCAGCAA | TGAAGATGAN | GAGGANGATG | AAGAAGAACG | TCNCGAGGGC | 420 |
| ACACTTGCTC | TCAGTCTTAN | CACCATANCA | GCCCNTGAAA | ACCAANANCA | AAGACCACNA | 480 |
| CNCCGGCTGC | GATGAAGAAA | TNACCCNCG | TTGACAACT | TGCATGGCAC | TGGGANCCAC | 540 |
| AGTGGCCCN | AAAATCTTCA | AAAAGGATGC | CCCATCNATT | GACCCCCCAA | ATGCCCACTG | 600 |
| CCAACAGGGG | CTGCCCCACN | CNCNNAACGA | TGANCCNATT | GNACAAGATC | TNCNTGGTCT | 660 |
| TNATNAACNT | GAACCCTGCN | TNGTGGCTCC | TGTTTCAGGNC | CNNGGCCTGA | CTTCTNAANN | 720 |
| AANGAACTCN | GAAGNCCCCA | CNGGANANNC | G | | | 751 |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| GAGCCAGGCG | TCCCTCTGCC | TGCCCCACTCA | GTGGCAACAC | CCGGGAGCTG | TTTTGTCCTT | 60 |
| TGTGGANCC | CAGCAGTNC | CTCTTTTCA | ACTCANTGCC | AAGANCCCTG | AACAGGAGCC | 120 |
| ACCATGCAGT | GCTTCAGCTT | CATTAAAGAC | ATGATGATCC | TCTTCAATTT | GCTCATCTTT | 180 |
| CTGTGTGGTG | CAGCCCTGTT | GGCAGTGGGC | ATCTGGGTGT | CAATCGATGG | GGCATCCTTT | 240 |
| CTGAAGATCT | TCGGGCCACT | GTCGTCCAGT | GCCATGCAGT | TTGTCAACGT | GGGCTACTTC | 300 |
| CTCATCGCAG | CCGGCGTTGT | GGTCTTAGCT | CTAGGTTTCC | TGGGCTGCTA | TGGTGCTAAG | 360 |
| ACTGAGAGCA | AGTGTGCCCT | CGTGACGTT | TTCTTCATCC | TCCTCCTCAT | CTTCATTGCT | 420 |
| GAGGTTGCAA | TGCTGTGGTC | GCCTTGGTGT | ACACCACAAT | GGCTGAGCAC | TTCTTGACGT | 480 |
| TGCTGGTAAT | GCCTGCCATC | AANAAAAGAT | TATGGGTTCC | CAGGAANACT | TCACTCAAGT | 540 |
| GTTGGAACAC | CACCATGAAA | GGGCTCAAGT | GCTGTGGCTT | CNNCCAATA | TACGGATTTT | 600 |
| GAAGANTCAC | CTACTTCAAA | GAAAANAGTG | CCTTTCCCCC | ATTTCTGTTG | CAATTGACAA | 660 |
| ACGTCCCCAA | CACAGCCAAT | TGAAAACCTG | CACCCAACCC | AAANGGGTCC | CCAACCANAA | 720 |
| ATTNAAGGG | | | | | | 729 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| TGCTCTTCCT | CAAAGTTGTT | CTTGTTGCCA | TAACAACCAC | CATAGGTAAA | GCGGGCGCAG | 60 |
| TGTTGCTGTA | AGGGGTTGTA | GTACCAGCGC | GGGATGCTCT | CCTTGACAG | TCCTGTGTCT | 120 |
| GGCAGGTCCA | CGCAGTGCCC | TTTGTCAC | TGGGAAATGGA | TGCGCTGGAG | CTCGTCAAAG | 180 |
| CCACTCGTGT | ATTTTTCACA | GGCAGCCTCG | TCCGACCGGT | CGGGGCAGTT | GGGGGTGTCT | 240 |
| TCACACTCCA | GGAAACTGTC | NATGCAGCAG | CCATTGCTGC | AGCGGAACTG | GGTGGGCTGA | 300 |
| CANGTGCCAG | AGCACACTGG | ATGGCGCCTT | TCCATGNNAN | GGGCCCTGNG | GGAAAGTCCC | 360 |
| TGANCCCCAN | ANCTGCCTCT | CAAANGCCCC | ACCTTGACAC | CCCCGACAGG | CTAGAATGGA | 420 |
| ATCTTCTTCC | CGAAAGGTAG | TTNTTCTTGT | TGCCCAANCC | ANCCCCNTAA | ACAAACTCTT | 480 |
| GCANATCTGC | TCCGNGGGGG | TCNTANTACC | ANCGTGGGAA | AAGAACCCCA | GGCNGCGAAC | 540 |
| CAANCTTGTT | TGGATNCGAA | GCNATAATCT | NCTNTTCTGC | TTGGTGGACA | GCACCANTNA | 600 |
| CTGTNNANCT | TTAGNCCNTG | GTCCTCNTGG | GTTGNNTTGT | AACCTAATCN | CCNNTCAACT | 660 |
| GGGACAAGGT | AANTNGCCNT | CCTTTNAATT | CCCNANCNTN | CCCCCTGGTT | TGGGGTTTTN | 720 |
| CNCNCTCCTA | CCCCAGAAAN | NCCGTGTTCC | CCCCCAACTA | GGGGCCNAAA | CCNNTTNTTC | 780 |
| CACAACCTTN | CCCCACCCAC | GGGTTGNGNT | GGTGTTNG | | | 816 |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CCAAGGCCTG | GGCAGGCATA | NACCTGAAGG | TACAACCCCA | GGAACCCCTG | GTGCTGAAGG | 60 |
| ATGTGGAAAA | CACAGATTGG | CGCCTACTGC | GGGGTGACAC | GGATGTCAGG | GTAGAGAGGA | 120 |
| AAGACCCAAA | CCAGGTGGAA | CTGTGGGGAC | TCAAGGAANG | CACCTACCTG | TTCCAGCTGA | 180 |
| CAGTGACTAG | CTCAGACCAC | CCAGAGGACA | CGGCCAACGT | CACAGTCACT | GTGCTGTCCA | 240 |
| CCAAGCAGAC | AGAAGACTAC | TGCCTCGCAT | CCAACAANGT | GGGTCGCTGC | CGGGGCTCTT | 300 |
| TCCACGCTG | GTACTATGAC | CCCACGGAGC | AGATCTGCAA | GAGTTTCGTT | TATGGAGGCT | 360 |
| GCTTGGGCAA | CAAGAACAAC | TACCTTCGGG | AAGAAGAGTG | CATTCTANCC | TGTCNNGGTG | 420 |
| TGCAAGGTGG | GCCTTTGANA | NGCANCTCTG | GGGCTCANGC | GACTTTCCCC | CAGGGCCCCCT | 480 |
| CCATGGAAAG | GCGCCATCCA | NTGTTCTCTG | GCACCTGTCA | GCCCACCCAG | TTCCGCTGCA | 540 |
| NCAATGGCTG | CTGCATCNAC | ANTTTCCTNG | AATTGTGACA | ACACCCCCCA | NTGCCCCCAA | 600 |
| CCCTCCCAAC | AAAGCTTCCC | TGTTNAAAAA | TACNCCANTT | GGCTTTTNAC | AAACNCCCGG | 660 |
| CNCCTCCNTT | TTCCCCNNTN | AACAAAGGGC | NCTNGCNTTT | GAAGTCCCN | AACCCNGGAA | 720 |
| TCTNCCNNGG | AAAAANTNCC | CCCCCTGGTT | CCTNNAANCC | CCTCCNCNAA | ANCTNCCCCC | 780 |
| CCC | | | | | | 783 |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| | | | | | | |
|------------|-------------|-------------|-------------|------------|-------------|-----|
| GCCCCAATTC | CAGCTGCCAC | ACCACCCACG | GTGACTGCAT | TAGTTCGGAT | GTCATACAAA | 60 |
| AGCTGATTGA | AGCAACCCCTC | TACTTTTGG | TCGTGAGCCT | TTTGCTTGGT | GCAGGTTTCA | 120 |
| TTGGCTGTGT | TGGTGACGTT | GTCATTGCAA | CAGAAATGGGG | GAAAGGCACT | GTTCTCTTTG | 180 |
| AAGTAGGGTG | AGTCCTCAAA | ATCCGTATAG | TTGGTGAAGC | CACAGCACTT | GAGCCCTTTC | 240 |
| ATGGTGGTGT | TCCACACTTG | AGTGAAGTCT | TCCTGGGAAC | CATAATCTTT | CTTGATGGCA | 300 |
| GGCACTACCA | GCAACGTCAG | GAAGTGCTCA | GCCATTGTGG | TGTACACCAA | GGCGACCACA | 360 |
| GCAGCTGCAA | CCTCAGCAAT | GAAGATGAGG | AGGAGGATGA | AGAAGAACGT | CNCGAGGGCA | 420 |
| CACTTGCTCT | CCGTCTTAGC | ACCATAGCAG | CCCANGAAAC | CAAGAGCAAA | GACCACAACG | 480 |
| CCNGCTGCGA | ATGAAAGAAA | NTACCCACGT | TGACAACTG | CATGGCCACT | GGACGACAGT | 540 |
| TGGCCCGAAN | ATCTTCAGAA | AAGGGATGCC | CCATCGATTG | AACACCCANA | TGCCCCACTGC | 600 |
| CNACAGGGCT | GCNCCNCNCN | GAAAGAATGA | GCCATTGAAG | AAGGATCNTC | NTGGTCTTAA | 660 |
| TGAAGTGAAG | CCNTGCATGG | TGGCCCCCTGT | TCAGGGCTCT | TGGCAGTGAA | TTCTGANAAA | 720 |
| AAGGAACNGC | NTNAGCCCCC | CCAAANGANA | AAACACCCCC | GGGTGTTGCC | CTGAATTGGC | 780 |
| GGCCAAGGAN | CCCTGCCCCN | G | | | | 801 |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTGAGAGCCA | GGCGTCCCTC | TGCCTGCCCA | CTCAGTGGCA | ACACCCGGGA | GCTGTTTTGT | 60 |
| CCTTTGTGGA | GCCTCAGCAG | TTCCCTCTTT | CAGAATCAC | TGCCAAGAGC | CCTGAACAGG | 120 |
| AGCCACCATG | CAGTGCTTCA | GCTTCATTAA | GACCATGATG | ATCCTCTTCA | ATTTGCTCAT | 180 |
| CTTTCTGTGT | GGTGCAGCCC | TGTTGGCAGT | GGGCATCTGG | GTGTCAATCG | ATGGGGCATC | 240 |
| CTTTCTGAAG | ATCTTCGGGC | CAGTGTCTGC | CAGTGCCATG | CAGTTTGTCA | ACGTGGGCTA | 300 |
| CTTCCTCATC | GCAGCCGGCG | TTGTGGTCTT | TGCTCTTGGT | TTCCTGGGCT | GCTATGGTGC | 360 |

| | |
|--|-----|
| TAAGACGGAG AGCAAGTGTG CCCTCGTGAC GTTCTTCTTC ATCCTCCTCC TCATCTTCAT | 420 |
| TGCTGAAGTT GCAGCTGCTG TGGTCGCCTT GGTGTACACC ACAATGGCTG AACCATTCCCT | 480 |
| GACGTTGCTG GTANTGCCTG CCATCAANAA AGATTATGGG TTCCCAGGAA AAATTCACTC | 540 |
| AANTNTGGAA CACCNCCATG AAAAGGGCTC CAATTCTGN TGGCTTCCCC AACTATACCG | 600 |
| GAATTTTGAA AGANTCNCCC TACTTCCAAA AAAAAANANT TGCCTTNCC CCCNTTCTGT | 660 |
| TGCAATGAAA ACNTCCCAAN ACNGCCAATN AAAACCTGCC CNNNCAAAAA GGNTCNCAAA | 720 |
| CAAAAAAANT NNAAGGGTTN | 740 |

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

| | |
|---|-----|
| CCGCTGGTTG CGCTGGTCCA GNGNAGCCAC GAAGCACGTC AGCATACACA GCCTCAATCA | 60 |
| CAAGGTCTTC CAGCTGCCGC ACATTACGCA GGGCAAGAGC CTCCAGCAAC ACTGCATATG | 120 |
| GGATACACTT TACTTTAGCA GCCAGGGTGA CAACTGAGAG GTGTCGAAGC TTATTCTTCT | 180 |
| GAGCCTCTGT TAGTGGAGGA AGATTCCGGG CTTCACTAA GTAGTCAGCG TATGTCCCAT | 240 |
| AAGCAAACAC TGTGAGCAGC CGGAAGGTAG AGGCAAAGTC ACTCTCAGCC AGCTCTCTAA | 300 |
| CATTGGGCAT GTCCAGCAGT TCTCCAAACA CGTAGACACC AGNGGCCTCC AGCACCTGAT | 360 |
| GGATGAGTGT GGCCAGCGCT GCCCCTTGG CCGACTTGGC TAGGAGCAGA AATTGCTCCT | 420 |
| GGTTCTGCCC TGTCACCTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG | 480 |
| GCTCAGGATG TCCAGAGACG TGTTCCGCC CCCTCNCTTA ATGACACCGN CCANNCAACC | 540 |
| GTCGGCTCCC GCCGANTGNG TTCGTCGTNC CTGGGTCAGG GTCTGCTGGC CNCTACTTGC | 600 |
| AANCTTCGTC NGGCCCCATG AATTCACCNC ACCGGAACNT GTANGATCCA CTNNTTCTAT | 660 |
| AACCGNCGC CACCGCNNNT GGAACCTCAC TCTTNTNCC TTTACTTGAG GGTAAAGGTC | 720 |
| ACCCCTNNCG TTACCTTGGT CCAAACNTN CCNTGTGTG ANATNGTNAA TCNGGNCCNA | 780 |
| TNCCANCCNC ATANGAAGCC NG | 802 |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | |
|---|-----|
| CNAAGCTTCC AGGTNACGGG CCGCNAANCC TGACCCNAGG TANCANAANG CAGNCNGCGG | 60 |
| GAGCCCACCG TCACGNGGNG GNGTCTTTAT NGGAGGGGGC GGAGCCACAT CNCTGGACNT | 120 |
| CNTGACCCCA ACTCCCCNCC NCNCANTGCA GTGATGAGTG CAGAAGTGAA GGTNACGTGG | 180 |
| CAGGAACCAA GANCAANNC TGCTCCNNTC CAAGTCGGCN NAGGGGGCGG GGCTGGCCAC | 240 |
| GCNCATCCNT CNAGTGCTGN AAAGCCCCNN CCTGTCTACT TGTTTGGAGA ACNGCNNNGA | 300 |
| CATGCCCAGN GTTANATAAC NGGCNGAGAG TNANTTTGCC TCTCCCTTCC GGCTGCGCAN | 360 |
| CGNGTNTGCT TAGNGGACAT AACCTGACTA CTTAACTGAA CCCNNGAATC TNCCNCCCCT | 420 |
| CCACTAAGCT CAGAACAAAA AACTTCGACA CCACTCANTT GTCACCTGNC TGCTCAAGTA | 480 |
| AAGTGTAACC CATNCCCAAT GTNTGCTNGA NGCTCTGNCC TGCNTTANGT TCGGTCTTGG | 540 |
| GAAGACCTAT CAATTNAAGC TATGTTTCTG ACTGCCTCTT GCTCCCTGNA ACAANCNACC | 600 |
| CNNCNTTCCA AGGGGGGGNC GGCCCCAAT CCCCCCAACC NTNAATTNAN TTTANCCCN | 660 |
| CCCCNNGGCC CGGCCTTTTA CNANCNTCN NACNNGGNA AAACCNNGC TTTNCCCAAC | 720 |
| NNAATCCNCC T | 731 |

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TAAAAACCCC | CTCCATTNAA | TGNAAACTTC | CGAAATTGTC | 60 |
| CAACCCCTC | NTCCAAATNN | CCNTTTCGG | GNGGGGGTTC | CAAACCCAAN | TTANNTTGG | 120 |
| ANNTTAAATT | AAATNTTNN | TGGNGGNNA | ANCCNAATGT | NANGAAAGTT | NAACCCANTA | 180 |
| TNANCTTNA | TNCCTGGAAA | CCNGTNGNTT | CCAAAAATNT | TTAACCCCTTA | ANTCCCTCCG | 240 |
| AAATNGTTNA | NGGAAAACCC | AANTTCTCNT | AAGGTTGTTT | GAAGGNTNAA | TNAAAANCCC | 300 |
| NNCCAATTGT | TTTTNGCCAC | GCCTGAATTA | ATTGGNTTCC | GNTGTTTTCC | NTTAAAAANAA | 360 |
| GGNNANCCCC | GGTTANTNAA | TCCCCCNCNC | CCCAATTATA | CCGANTTTTT | TTNGAATTGG | 420 |
| GANCCNCNCG | GAATTAACGG | GGNNNNTCCC | TNTTGGGGGG | CNGGNNCCCC | CCCCNTCGGG | 480 |
| GGTTNGGGNC | AGGNCNNAAT | TGTTTAAAGG | TCCGAAAAAT | CCCTCCNAGA | AAAAANCTC | 540 |
| CCAGGNTGAG | NNTNGGGTTT | NCCCCCCCC | CANGGCCCT | CTCGNANAGT | TGGGGTTTGG | 600 |
| GGGGCTGGG | ATTTTNTTTC | CCCTNTTNCC | TCCCCCCCC | CCNGGGANAG | AGGTTNGNGT | 660 |
| TTTGNTCNC | GGCCCCNCCN | AAGANCTTTN | CCGANTTNAN | TTAAATCCNT | GCCTNGGCGA | 720 |
| AGTCNTTGN | AGGGNTAAAN | GGCCCCCTNN | CGGG | | | 754 |

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | | | | | | | | |
|------------|------------|---|------------|----|------------|------------|------------|-----|
| ATCANCCCAT | GACCCCNAA | C | NGGGACCC | NC | TCANCCGGNC | NNNCNACCNC | CGGCCNATCA | 60 |
| NNGTNAGNNC | ACTNCNNTN | N | NATCACNCCC | C | CNCCNACTAC | GCCNCNANC | CNACGCNCTA | 120 |
| NNCANATNCC | ACTGANNGCG | C | CGANGTNGAN | N | NGAGAAANCT | NATACCANAG | NCACCANACN | 180 |
| CCAGCTGTCC | NANAANGCCT | N | NNNATACNGG | N | NNNATCCAAT | NTGNANCCTC | CNAAGTATTN | 240 |
| NNCNANANAT | GATTTTCCTN | A | ANCCGATTAC | C | CCNTNCCCCC | TANCCCCCTC | CCCCAACNA | 300 |
| CGAAGGCNCT | GGNCCNAAG | G | NGGCGNCNCC | C | CCGCTAGNTC | CCCNCAAGT | CNCNCNCCTA | 360 |
| AACTCANCCN | NATTACNCGC | T | TTCNTGAGTA | T | CACTCCCCCG | AATCTCACCC | TACTCAACTC | 420 |
| AAAAANATCN | GATACAAAAT | A | AATNCAAGCC | T | GNATTATNAC | ACTNTGACTG | GGTCTCTATT | 480 |
| TTAGNGGTCC | NTNAANCNTC | C | TAATACTTC | C | AGTCTNCCCT | TCNCCAATTT | CCNAANGGCT | 540 |
| CTTTCNGACA | GCAINTTTTG | G | TTCCCNNTT | G | GGTTCCTTAN | NGAATTGCC | TTCNTNGAAC | 600 |
| GGGCTCNTCT | TTTCCTTCGG | T | TANCTTGGN | T | TCNNCCGGC | CAGTTATTAT | TTCCNTTTT | 660 |
| AAATTCNTNC | CNTTTANTTT | T | TGCNTTCNA | A | AACCCCGGC | CTTGAAAACG | GCCCCCTGGT | 720 |
| AAAAGTTGT | TTTGANAAAA | T | TTTTGTTTT | G | TTC | | | 755 |

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 849 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTANGTG | TNGTCGTGCA | GGTAGAGGCT | TACTACAANT | GTGAANACGT | 60 |
| ACGCTNGGAN | TAANGCGACC | CGANTTCTAG | GANNCNCCCT | AAAATCANAC | TGTGAAGATN | 120 |
| ATCCTGNNNA | CGGAANGGTC | ACCGGNNGAT | NNTGCTAGGG | TGNCCNCTCC | CANNNCNTTN | 180 |
| CATAACTCNG | NGGCCCTGCC | CACCACCTTC | GGCGGCCCN | NGNCCGGGCC | CGGGTCATTN | 240 |
| GNNTTAACCN | CACTNNGCNA | NCGGTTTCN | NCCCCNCCNG | ACCCNGGCCA | TCCGGGGTNC | 300 |
| TCTGTCTTCC | CCTGNAGNCN | ANAAANTGGG | CCNCGNCCC | CTTTACCCCT | NNACAAGCCA | 360 |
| CNGCCNTCTA | NCCNCNGCCC | CCCCTCCANT | NNGGGGGACT | GCCNANNGCT | CCGTTNCTNG | 420 |
| NNACCCCN | GGGTNCCTCG | GTTGTCGANT | CNACCGNANG | CCANGGATTC | CNAAGGAAGG | 480 |
| TGCGTTNTTG | GGCCCTACCC | TTCGCTNCGG | NNCACCTTC | CCGACNANGA | NCCGCTCCCG | 540 |
| CNCNCGNNG | CCTCNCCTCG | CAACACCCGC | NCTCNTNGT | NCGGNNNCCC | CCCCACCCGC | 600 |
| NCCCTCNCNC | NGNCGNANCN | CTCCNCCNCC | GTCTCANCA | CCACCCGCC | CCGCCAGGCC | 660 |
| NTCANCCACN | GGNNGACNNG | NAGCNCNNTC | GCNCCGCGCN | GCGNCCCT | CGCNCNGAA | 720 |
| CTNCNTCNGG | CCANTNNGCG | TCAANCCNNA | CNAAACGCCG | CTGCGCGGCC | CGNAGCGNCC | 780 |
| NCCTCCNCGA | GTCTCCCGN | CTTCNACCC | ANGNNTTCN | CGAGGACACN | NNACCCGCC | 840 |
| NNCANGCGG | | | | | | 849 |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 872 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCGCAAATA | TACTTCGCTC | GNACTCGTGC | GCCTCGCTNC | TCTTTTCCTC | CGCAACCATG | 60 |
| TCTGACNANC | CCGATTNNGC | NGATATCNAN | AAGNTCGANC | AGTCCAAACT | GANTAACACA | 120 |
| CACACNANAN | AGANAAATCC | NCTGCCTTCC | ANAGTANACN | ATTGAACNNG | AGAACCANGC | 180 |
| NGGCGAATCG | TAATNAGGCG | TGCGCCGCCA | ATNTGTCNCC | GTTTATTNTN | CCAGCNTCNC | 240 |
| CTNCCNACCC | TACNTCTTCN | NAGCTGTCNN | ACCCCTNGTN | CGNACCCCCC | NAGGTCGGGA | 300 |
| TCGGGTTTNN | NNTGACCGNG | CNNCCCCCTC | CCCCNTCCAT | NACGANCCNC | CCGCACCACC | 360 |
| NANNGCNCGC | NCCCCGNNCT | CTTCGCCNCC | CTGTCCTNTN | CCCCTGTNGC | CTGGCNCNGN | 420 |
| ACCGCATTGA | CCCTCGCCNN | CTNCNNGAAA | NCGNANACGT | CCGGGTTGNN | ANNANCGCTG | 480 |
| TGGGNNNGCG | TCTGCNCCGC | GTTCTTCCN | NCNNTTCCA | CCATCTTCNT | TACNNGGTCT | 540 |
| CCNCGCCNTC | TCNNNCACNC | CCTGGGACGC | TNTCTNTGTC | CCCCCTTNAC | TCCCCCCTT | 600 |
| CGNCGTGNC | CGNCCCCACC | NTCATTNTCA | NACGNTCTTC | ACAANNNCCT | GGNTNNTCTC | 660 |
| CNANCNGNCN | GTCANCCNAG | GGAAGGNGG | GGNNCCNNTG | NTTGACGTTG | NGGNGANGTC | 720 |
| CGAANANTCC | TCNCCNTCAN | CNCTACCCCT | CGGGCGNNCT | CTCNGTTNCC | AACTTANCAA | 780 |
| NTCTCCCCCG | NGNGCNCNTC | TCAGCCTCNC | CCNCCCCNCT | CTCTGCANTG | TNCTCTGCTC | 840 |
| TNACCNTTAC | GANTNTTCGN | CNCCCTCTTT | CC | | | 872 |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GCATGCAAGC | TTGAGTATTC | TATAGNGTCA | CCTAAATANC | TTGGCNTAAT | CATGGTCNTA | 60 |
| NCTGNCTTCC | TGTGTCAAAT | GTATACNAAN | TANATATGAA | TCTNATNTGA | CAAGANNNGTA | 120 |

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| TCNTNCATTA | GTAACAANTG | TNNTGTCCAT | CCTGTCNGAN | CANATTCCCA | TNNATTNCGN | 180 |
| CGCATTNCN | GCNCANTATN | TAATNGGGAA | NTCNNNTNNN | NCACCNNCAT | CTATCNTNCC | 240 |
| GCNCCCTGAC | TGGNAGAGAT | GGATNANTTC | TNNTNTGACC | NACATGTTCA | TCTTGGATTN | 300 |
| AANANCCCCC | CGCNGNCCAC | CGGT'TNGNNG | CNAGCCNNTC | CCAAGACCTC | CTGTGGAGGT | 360 |
| AACCTGCGTC | AGANNCATCA | AACNTGGGAA | ACCCGCNNCC | ANGTNNAAGT | NGNNNCANAN | 420 |
| GATCCCGTCC | AGGNTTNACC | ATCCCTTCNC | AGCGCCCCCT | TTNGTGCCTT | ANAGNGNAGC | 480 |
| GTGTCCNANC | CNCTCAACAT | GANACGCGCC | AGNCCANCCG | CAATTNGGCA | CAATGTGCGC | 540 |
| GAACCCCTTA | GGGGGANTNA | TNCAAANCCC | CAGGATTGTC | CNCNCANGAA | ATCCCNCAAC | 600 |
| CCCNCCCTAC | CCNCTTTTGG | GACNGTGACC | AANTCCCGGA | GTNCCAGTCC | GGCCNGNCTC | 660 |
| CCCCACCGGT | NNCNTGGGG | GGGTGAANCT | CNGNNTCANC | CNGNCGAGGN | NTCGNAAGGA | 720 |
| ACCGGNCCTN | GGNCGAANNG | ANCNNTCNGA | AGNGCCNCNT | CGTATAACCC | CCCCCNCCA | 780 |
| NCCNACNGNT | AGNTCCCCC | CNGGGTNCGG | AANGG | | | 815 |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 775 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCGAGATGTC | TCGCTCCGTG | GCCTTAGCTG | TGCTCGCGCT | ACTCTCTCTT | TCTGGCCTGG | 60 |
| AGGCTATCCA | GCGTACTCCA | AAGATTCAAG | TTTACTCACG | TCATCCAGCA | GAGAATGGAA | 120 |
| AGTCAAATTT | CCTGAATTGC | TATGTGTCTG | GGTTTCATCC | ATCCGACATT | GAANTTGACT | 180 |
| TACTGAAGAA | TGGANAGAGA | ATTGAAAAAG | TGGAGCATTC | AGACTTGTCT | TTCAGCAAGG | 240 |
| ACTGGTCTTT | CTATCTCNTG | TACTACACTG | AATTCAACCC | CACTGAAAAA | GATGAGTATG | 300 |
| CCTGCCGTGT | GAACCATGTG | ACTTTGTCTC | AGCCCAAGAT | AGTTAAGTGG | GATCGAGACA | 360 |
| TGTAAGCAGN | CNNCATGGAA | GTTTGAAGAT | GCCGCATTTC | GATTGGATGA | ATTCCAAATT | 420 |
| CTGCTTGCTT | GCNTTTTAAT | ANTGATATGC | NTATACACCC | TACCTTTTAT | GNCCCCAAAT | 480 |
| TGTAGGGGTT | ACATNANTGT | TCNCNTNGGA | CATGATCTTC | CTTTATAANT | CCNCCNTTCG | 540 |
| AATTGCCCGT | CNCCNGTTN | NGAATGTTTC | CNNAACCACG | GTTGGCTCCC | CCAGGTCNCC | 600 |
| TCTTACGGAA | GGGCCTGGGC | CNCTTTNCAA | GGTTGGGGGA | ACCNAAAATT | TCNCTTNTGC | 660 |
| CCNCCNCCA | CNNTCTTGNG | NNCNCANTTT | GGAACCTTTC | CNATTCCCTT | TGGCCTCNNA | 720 |
| NCCTTNNTA | ANAAAACTTN | AAANCGTNGC | NAAANNTTTN | ACTTCCCCC | TTACC | 775 |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ANATTANTAC | AGTGTAATCT | TTTCCCAGAG | GTGTGTANAG | GGAACGGGGC | CTAGAGGCAT | 60 |
| CCCANAGATA | NCTTATANCA | ACAGTGCTTT | GACCAAGAGC | TGCTGGGCAC | ATTTCTTGCA | 120 |
| GAAAAGGTGG | CGGTCCCAT | CACTCCTCCT | CTCCCATAGC | CATCCCAGAG | GGGTGAGTAG | 180 |
| CCATCANGCC | TTGGGTGGGA | GGGAGTCANG | GAAACAACAN | ACCACAGAGC | ANACAGACCA | 240 |
| NTGATGACCA | TGGGCGGGAG | CGAGCCTCTT | CCCTGNACCG | GGGTGGCANA | NGANAGCCTA | 300 |
| NCTGAGGGGT | CACACTATAA | ACGTTAACGA | CCNAGATNAN | CACCTGCTTC | AAGTGCACCC | 360 |
| TTCTTACCTG | ACNACCAGNG | ACNNNNAACT | GCNGCCTGGG | GACAGCNCTG | GGANCAGCTA | 420 |
| ACNNAGCACT | CACCTGCCCC | CCCATGGCCG | TNCGCNTCCC | TGGTCCTGNC | AAGGGAAGCT | 480 |
| CCCTGTTGGA | ATTNCGGGGA | NACCAAGGGA | NCCCCCTCCT | CCANCTGTGA | AGGAAAAANN | 540 |
| GATGGAATTT | TNCCCTTCCG | GCCNNTCCCC | TCTTCCTTTA | CACGCCCCCT | NNTACTCNTC | 600 |

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TCCCTCTNTT | NTCCTGNCNC | ACTTTTNACC | CCNNNATTTC | CCTTNATTGA | TCGGANNCTN | 660 |
| GANATTCCAC | TNNCGCCTNC | CNTCNATCNG | NAANACNAAA | NACTNTCTNA | CCNNGGGGAT | 720 |
| GGGNCCCTCG | NTCATCCTCT | CTTTTTCNCT | ACCNCCNNTT | CTTTGCCTCT | CCTTNGATCA | 780 |
| TCCAACNCNTC | GNTGGCCNTN | CCCCCCCNNN | TCCTTTNCCC | | | 820 |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| TCTGGGTGAT | GGCCTCTTCC | TCCTCAGGGA | CCTCTGACTG | CTCTGGGCCA | AAGAATCTCT | 60 |
| TGTTTCTTCT | CCGAGCCCCA | GGCAGCGGTG | ATTGAGCCCT | GCCCAACCTG | ATTCTGATGA | 120 |
| CTGCGGATGC | TGTGACGGAC | CCAAGGGGCA | AATAGGGTCC | CAGGGTCCAG | GGAGGGGCGC | 180 |
| CTGCTGAGCA | CTTCCGCCCC | TCACCCTGCC | CAGCCCCTGC | CATGAGCTCT | GGGCTGGGTC | 240 |
| TCCGCCTCCA | GGTTTCTGCT | CTTCCANGCA | NGCCANCAAG | TGGCGCTGGG | CCACACTGGC | 300 |
| TTCTTCCTGC | CCCNTCCCTG | GCTCTGANTC | TCTGTCTTCC | TGTCCTGTGC | ANGCNCCTTG | 360 |
| GATCTCAGTT | TCCCTCNCCTC | ANNGAACTCT | GTTTCTGANN | TCTTCANTTA | ACTNTGANTT | 420 |
| TATNACCNAN | TGGNCTGTNC | TGTCNNACTT | TAATGGGCCN | GACCGGCTAA | TCCCTCCCTC | 480 |
| NCTCCCTTCC | ANTTCNNNNA | ACCNGCTTNC | CNTCNTCTCC | CCNTANCCCG | CCNNGGAANC | 540 |
| CTCCTTTGCC | CTNACCANGG | GCCNNNACCG | CCCNNTNCTN | GGGGGGCNNG | GTNNCTNCNC | 600 |
| CTGNTNNCCC | CNCTCNCNNT | TNCCTCGTCC | CNNCNCNCGN | NNGCANNTTC | NCNGTCCCN | 660 |
| TNNCTCTTCN | NGTNTCGNAA | NGNTCNCNTN | TNNNNNGNCN | NGNTNNTNCN | TCCCTCTCNC | 720 |
| CNNNTGNANG | TNNTTNNNNC | NCNGNNCCCC | NNNNCNNNNN | NGGNNNTNNN | TCTNCNCNGC | 780 |
| CCCNCCCCC | NGNATTAAGG | CCTCCNNTCT | CCGGCCNC | | | 818 |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| AGGAAGGGCG | GAGGGATATT | GTANGGGATT | GAGGGATAGG | AGNATAANGG | GGGAGGTGTG | 60 |
| TCCCAACATG | ANGGTGNNGT | TCTCTTTTGA | ANGAGGGTTG | NGTTTTTANN | CCNNGTGGGT | 120 |
| GATTNAACCC | CATTGTATGG | AGNNAAAGGN | TTTNAGGGAT | TTTTCGGCTC | TTATCAGTAT | 180 |
| NTANATTCTT | GTNAATCGGA | AAATNATNTT | TCNNCNGGAA | AATNTTGCTC | CCATCCGNAA | 240 |
| ATTNCTCCCG | GGTAGTGCA | NTTNGGGGGN | CNGCCANGTT | TCCCAGGCTG | CTANAATCGT | 300 |
| ACTAAAGNTT | NAAGTGGGAN | TNCAAATGAA | AACCTNNCAC | AGAGNATCCN | TACCCGACTG | 360 |
| TNNNTTNCCT | TCGCCCTNTG | ACTCTGCNNG | AGCCCCAATAC | CCNNGNGNAT | GTNCCCCNGN | 420 |
| NNNGCGNCNC | TGAAANNNNC | TCGNGGCTNN | GANCATCANG | GGGTTTCGCA | TCAAAAGCNC | 480 |
| CGTTTCNCAT | NAAGGCACTT | TNGCCTCATC | CAACCNTNG | CCCTCNCNCA | TTTNGCCGTC | 540 |
| NGGTTNCNCT | ACGCTNNTNG | CNCCTNNNTN | GANATTTTNC | CCGCCTNGGG | NAANCCTCCT | 600 |
| GNAATGGGTG | GGGNCCTTTC | TTTTNACCNN | GNGGTNTACT | AATCNCNTNC | ACGCNTNCTT | 660 |
| TCTCNACCCC | CCCCCTTTT | CAATCCCANC | GGCNAATGGG | GTCTCCCCNN | CGANGGGGGG | 720 |
| NNNCCCANN | C | | | | | 731 |

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| ACTAGTCCAG | TGTGGTGGAA | TTCCATTGTG | TTGGGGNCNC | TTCTATGANT | ANTNTTAGAT | 60 |
| CGCTCANACC | TCACANCTC | CCNACNANGC | CTATAANGAA | NANNAATAGA | NCTGTNCNNT | 120 |
| ATNTNTACNC | TCATANNCT | CNNNACCCAC | TCCCTCTTAA | CCCNTACTGT | GCCTATNGCN | 180 |
| TNNCTANTCT | NTGCCGCCTN | CNANCCACCN | GTGGGCCNAC | CNCNNGNATT | CTCNATCTCC | 240 |
| TCNCCATNTN | GCCTANANTA | NGTNCATACC | CTATACCTAC | NCCAATGCTA | NNNCTAANCN | 300 |
| TCCATNANTT | ANNNTAACTA | CCACTGACNT | NGACTTTTNC | ATNANCTCCT | AATTTGAATC | 360 |
| TACTCTGACT | CCCACNGCCT | ANNNATTAGC | ANCNTCCCCC | NACNATNTCT | CAACCAAATC | 420 |
| NTCAACAACC | TATCTANCTG | TTCNCCAACC | NTTNCCTCCG | ATCCCCNNAC | AACCCCCCTC | 480 |
| CCAAATACCC | NCCACCTGAC | NCCTAACCCN | CACCATCCCC | GCAAGCCNAN | GGNCATTAN | 540 |
| CCACTGGAAT | CACNATNGGA | NAAAAAAAC | CCNAACTCTC | TANCNCNNAT | CTCCCTAANA | 600 |
| AATNCTCCTN | NAATTTACTN | NCANTNCCAT | CAANCCCCACN | TGAAACNNAA | CCCCTGTTTT | 660 |
| TANATCCCTT | CTTTCGAAAA | CCNACCCCTT | ANNNCCCAAC | CTTNGGGGCC | CCCCCNCTNC | 720 |
| CCNAATGAAG | GNCNCCCAAT | CNANGAAACG | NCCNTGAAAA | ANCNAGGCNA | ANANNNTCCG | 780 |
| CANATCCTAT | CCCTTANTTN | GGGGNCCCTT | NCCNGGGGCC | CC | | 822 |

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 787 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| CGGCCGCCTG | CTCTGGCACA | TGCCTCCTGA | ATGGCATCAA | AAGTGATGGA | CTGCCCATTG | 60 |
| CTAGAGAAGA | CCTTCTCTCC | TACTGTCAAT | ATGGAGCCCT | GCAGACTGAG | GGCTCCCCCT | 120 |
| GTCTGCAGGA | TTTGATGTCT | GAAGTCGTGG | AGTGTGGCTT | GGAGCTCCTC | ATCTACATNA | 180 |
| GCTGGAAGCC | CTGGAGGGCC | TCTCTCGCCA | GCCTCCCCCT | TCTCTCCACG | CTCTCCANGG | 240 |
| ACACCAGGGG | CTCCAGGCAG | CCCATTATTC | CCAGNANGAC | ATGGTGTTTC | TCCACGCGGA | 300 |
| CCCATGGGGC | CTGNAAGGCC | AGGGTCTCCT | TTGACACCAT | CTCTCCCGTC | CTGCCTGGCA | 360 |
| GGCCGTGGGA | TCCACTANTT | CTANAACGGN | CGCCACCNCG | GTGGGAGCTC | CAGCTTTTGT | 420 |
| TCCNTTAAT | GAAGGTTAAT | TGCNCGCTTG | GCCTAATCAT | NGGTCANAAC | TNTTTCCTGT | 480 |
| GTGAAATTGT | TTNTCCCCTC | NCNATTCCNC | NCNACATAACN | AACCCGGAAN | CATAAAGTGT | 540 |
| TAAAGCCTGG | GGGTNGCCTN | NNGAATNAAC | TNAACTCAAT | TAATTGCGTT | GGCTCATGGC | 600 |
| CCGCTTTCN | TTCNGAAAA | CTGTCNTCCC | CTGCNTTNNT | GAATCGGCCA | CCCCCNNGGG | 660 |
| AAAAGCGGTT | TGCNTTTTNG | GGGGNTCCTT | CCNCTTCCCC | CCTCNCTAAN | CCCTNCGCCT | 720 |
| CGGTCGTTNC | NGGTNGCGGG | GAANGGGNAT | NNNCTCCNC | NAAGGGGGNG | AGNNNGNTAT | 780 |
| CCCCAAA | | | | | | 787 |

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 799 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| TTTTTTTTTT | TTTTTTTGGC | GATGCTACTG | TTTAATTGCA | GGAGGTGGGG | GTGTGTGTAC | 60 |
| CATGTACCAG | GGCTATTAGA | AGCAAGAAGG | AAGGAGGGAG | GGCAGAGCGC | CCTGCTGAGC | 120 |
| AACAAAGGAC | TCCTGCAGCC | TTCTCTGTCT | GTCTCTTGGC | GCAGGCACAT | GGGGAGGCCCT | 180 |
| CCCGCAGGGT | GGGGGCCACC | AGTCCAGGGG | TGGGAGCACT | ACANGGGGTG | GGAGTGGGTG | 240 |
| GTGGCTGGTN | CNAATGGCCT | GNCACANATC | CCTACGATTC | TTGACACCTG | GATTTCACCA | 300 |
| GGGGACCTTC | TGTTCTCCCA | NGGNAACTTC | NTNNATCTCN | AAAGAACACA | ACTGTTTCTT | 360 |
| CNGCANTTCT | GGCTGTTTAT | GGAAAGCACA | GGTGTCCNAT | TTNGGCTGGG | ACTTGGTACA | 420 |
| TATGGTTCCG | GCCCACCTCT | CCCNTCNAAN | AAGTAATCA | CCCCCCCCCN | CCNTCTNTTG | 480 |
| CCTGGGCCCT | TAANTACCCA | CACCGGAATC | CANTTANTTA | TTCATCTTNG | GNTGGGCTTG | 540 |
| NTNATCNCCN | CCTGAANGCG | CCAAGTTGAA | AGGCCACGCC | GTNCCCNCTC | CCCATAGNAN | 600 |
| NTTTTNNCNT | CANCTAATGC | CCCCCNGGC | AACNATCCAA | TCCCCCCCCN | TGGGGGCCCC | 660 |
| AGCCCANGGC | CCCCGNTCTG | GGNNNCCNGN | CNCGNANTCC | CCAGGNTCTC | CCANTCNGNC | 720 |
| CCNNNGCNCC | CCCGCACGCA | GAACANAAGG | NTNGAGCCNC | CGCANNNNNN | NGGTNNCNAC | 780 |
| CTCGCCCCCC | CCNCGNNG | | | | | 799 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | 60 |
| TTTTNCCNAG | GGCAGGTTTA | TTGACAACCT | CNCGGGACAC | AANCAGGCTG | GGGACAGGAC | 120 |
| GGCAACAGGC | TCCGGCGGCG | GCGGCGGCGG | CCCTACCTGC | GGTACCAAAT | NTGCAGCCTC | 180 |
| CGCTCCCGCT | TGATNTTCCT | CTGCAGCTGC | AGGATGCCNT | AAAACAGGGC | CTCGGCCNTN | 240 |
| GGTGGGCACC | CTGGGATTIN | AATTTCCACG | GGCACAATGC | GGTCGCANCC | CCTCACCACC | 300 |
| NATTAGGAAT | AGTGGTNTTA | CCNCCNCCG | TTGGCNCAC | CCCNTGGAA | ACCACTTNTC | 360 |
| GCGGCTCCGG | CATCTGGTCT | TAAACCTTGC | AAACNCTGGG | GCCCTCTTTT | TGGTTANTNT | 420 |
| NCCNGCCACA | ATCATNACTC | AGACTGGCNC | GGGCTGGCCC | CAAAAAANCN | CCCCAAAACC | 480 |
| GGNCCATGTC | TTNNCGGGGT | TGCTGCNATN | TNCATCACCT | CCCGGGCNCA | NCAGGNCAAC | 540 |
| CCAAAAGTTC | TTNGGGCCCN | CAAAAAANCT | CCGGGGGGNC | CCAGTTTCAA | CAAAGTCATC | 600 |
| CCCCTTGGCC | CCCAAATCCT | CCCCCGGNTT | NCTGGGTTTG | GGAACCCACG | CCTCTNNCTT | 660 |
| TGGNNGGCAA | GNTGGNTCCC | CCTTCGGGCC | CCCGGTGGGC | CCNNCTCTAA | NGAAAACNCC | 720 |
| NTCCTNNNCA | CCATCCCCCC | NNGNNACGNC | TANCAANGNA | TCCCTTTTTT | TANAAACGGG | 780 |
| CCCCCNCG | | | | | | 789 |

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GACAGAACAT | GTTGGATGGT | GGAGCACCTT | TCTATACGAC | TTACAGGACA | GCAGATGGGG | 60 |
| AATTCATGGC | TGTTGGAGCA | ATANAACCCC | AGTTCTACGA | GCTGCTGATC | AAAGGACTTG | 120 |
| GACTAAAGTC | TGATGAACTT | CCCAATCAGA | TGAGCATGGA | TGATTGGCCA | GAAATGAANA | 180 |
| AGAAGTTTGC | AGATGTATTT | GCAAAGAAGA | CGAAGGCAGA | GTGGTGTCAA | ATCTTTGACG | 240 |
| GCACAGATGC | CTGTGTGACT | CCGGTTCTGA | CTTTTGAGGA | GGTTGTTTAT | CATGATCACA | 300 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACAANGAACG | GGGCTCGTTT | ATCACCANTG | AGGAGCAGGA | CGTGAGCCCC | CGCCCTGCAC | 360 |
| CTCTGCTGTT | AAACACCCCA | GCCATCCCTT | CTTTCAAAAG | GGATCCACTA | CTTCTAGAGC | 420 |
| GGNCGCCACC | GCGGTGGAGC | TCCAGCTTTT | GTTCCCTTTA | GTGAGGGTTA | ATTGCCGCGT | 480 |
| TGGCGTAATC | ATGGTCATAN | CTGTTCCTG | TGTGAAATTG | TTATCCGCTC | ACAATTCCAC | 540 |
| ACAACATACG | ANCCGGAAGC | ATNAAATTTT | AAAGCCTGGN | GGTNGCCTAA | TGANTGAACT | 600 |
| NACTCACATT | AATTGGCTTT | GCGCTCACTG | CCCGCTTTCC | AGTCCGGAAG | ACCTGTCCTT | 660 |
| GCCAGCTGCC | NTAATGAAT | CNGGCCACCC | CCCGGGGAAA | AGGCNGTTTG | CTTNTTGGGG | 720 |
| CGCNCTTCCC | GCTTCTCGC | TTCCTGAANT | CCTTCCCCCC | GGTCTTTCGG | CTTGCGGCNA | 780 |
| ACGGTATCNA | CCT | | | | | 793 |

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCCGCGACCG | GCATGTACGA | GCAACTCAAG | GGCGAGTGGA | ACCGTAAAAG | CCCCAATCTT | 60 |
| ANCAAGTGCG | GGGAANAGCT | GGGTCGACTC | AAGCTAGTTC | TTCTGGAGCT | CAACTTCTTG | 120 |
| CCAACCACAG | GGACCAAGCT | GACCAAACAG | CAGCTAATTC | TGGCCCGTGA | CATACTGGAG | 180 |
| ATCGGGGCCC | AATGGAGCAT | CCTACGCAAN | GACATCCCTT | CCTTCGAGCG | CTACATGGCC | 240 |
| CAGCTCAAAT | GCTACTACTT | TGATTACAAN | GAGCAGCTCC | CCGAGTCAGC | CTATATGCAC | 300 |
| CAGCTCTTGG | GCCTCAACCT | CCTCTTCCTG | CTGTCCCAGA | ACCGGGTGGC | TGANTNCCAC | 360 |
| ACGGANTTGG | ANCGGCTGCC | TGCCCAANGA | CATACANACC | AATGTCTACA | TCNACCACCA | 420 |
| GTGTCTTGG | GCAATACTGA | TGGANGGCAG | CTACCNCAA | GTNTTCCTGG | CCNAGGGTAA | 480 |
| CATCCCCCGC | CGAGAGCTAC | ACCTTCTTCA | TTGACATCCT | GCTCGACACT | ATCAGGGATG | 540 |
| AAAAATCGNG | GGTTGCTCCA | GAAAGGCTNC | AANAANATCC | TTTCNCTGA | AGGCCCCCGG | 600 |
| ATNCNCTAGT | NCTAGAAATC | GCCCGCCATC | GCGGTGGANC | CTCCAACCTT | TCGTTNCCCT | 660 |
| TTACTGAGGG | TTNATTGCCG | CCCTTGCGGT | TATCATGGTC | ACNCCNGTTN | CCTGTGTGTA | 720 |
| AATTNTTAAC | CCCCACAAT | TCCACGCCNA | CATTNG | | | 756 |

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGGGATCTCT | ANATCNACCT | GNATGCATGG | TGTGCGGTGT | GGTCGCTGTC | GATGAANATG | 60 |
| AACAGGATCT | TGCCCTTGAA | GCTCTCGGCT | GCTGTNTTTA | AGTTGCTCAG | TCTGCCGTCA | 120 |
| TAGTCAGACA | CNCTCTTGGG | CAAAAAACAN | CAGGATNTGA | GTCTTGATTT | CACCTCCAAT | 180 |
| AATCTTCNGG | GCTGTCTGCT | CGGTGAATC | GATGACNANG | GGCAGCTGGT | TGTGTNTGAT | 240 |
| AAANTCCANC | ANGTCTCTCT | TGGTGACCTC | CCCTTCAAAG | TTGTTCCGGC | CTTCATCAAA | 300 |
| CTTCTNNAAN | ANGANNANCC | CANCTTTGTC | GAGCTGGNAT | TTGGANAACA | CGTCACTGTT | 360 |
| GGAAACTGAT | CCCAAATGGT | ATGTCATCCA | TCGCCTCTGC | TGCCTGCAAA | AAACTTGCTT | 420 |
| GGCNCAAATC | CGACTCCCN | TCCTTGAAAG | AAGCCNATCA | CACCCCCCTC | CCTGGACTCC | 480 |
| NNCAANGACT | CTNCCGCTNC | CCCNTCCNNG | CAGGGTTGGT | GGCANNCCGG | GCCCNTGCGC | 540 |
| TTCTTCAGCC | AGTTACACAT | NTTCATCAGC | CCCTCTGCCA | GCTGTNTAT | TCCTTGGGGG | 600 |
| GGAANCCGTC | TCTCCCTTCC | TGAANNAACT | TTGACCGTNG | GAATAGCCGC | GCNTCNCCNT | 660 |
| ACNTNCTGGG | CCGGGTTCAA | ANTCCCTCCN | TTGNCNNTCN | CCTCGGGCCA | TTCTGGATTT | 720 |
| NCCNAACTTT | TTCCTTCCCC | CNCCCNCCG | NGTTTGGNTT | TTTCATNGGG | CCCCAACTCT | 780 |

GCTNTTGGCC ANTCCCCTGG GGGCNTNTAN CNCCCCCTNT GGTCCCNTNG GGCC

834

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGNCGCTTT | CCNGCCGCGC | CCCGTTTCCA | TGACNAAGGC | TCCCTTCANG | TTAAATACNN | 60 |
| CCTAGNAAAC | ATTAATGGGT | TGCTCTACTA | ATACATCATA | CNAACCAGTA | AGCCTGCCCA | 120 |
| NAACGCCAAC | TCAGGCCATT | CCTACCAAAG | GAAGAAAGGC | TGGTCTCTCC | ACCCCTGTGA | 180 |
| GGAAAGGCCT | GCCTTGTAAG | ACACCACAAT | NCGGCTGAAT | CTNAAGTCTT | GTGTTTTACT | 240 |
| AATGGAAAAA | AAAAATAAAC | AANAGGTTTT | GTTCTCATGG | CTGCCCACCG | CAGCCTGGCA | 300 |
| CTAAACANC | CCAGCGCTCA | CTTCTGCTTG | GANAAATATT | CTTTGCTCTT | TTGGACATCA | 360 |
| GGCTTGATGG | TATCACTGCC | ACNTTTCAC | CCAGCTGGGC | NCCCTTCCCC | CATNTTGTG | 420 |
| ANTGANCTGG | AAGGCCTGAA | NCTTAGTCTC | CAAAAGTCTC | NGCCCACAAG | ACCGGCCACC | 480 |
| AGGGGANGTC | NTTNCAGTG | GATCTGCCAA | ANANTACCCN | TATCATCNNT | GAATAAAAAG | 540 |
| GCCCCGAAC | GANATGCTTC | CANCANCTT | TAAGACCCAT | AATCCTNGAA | CCATGGTGCC | 600 |
| CTTCCGTCT | GATCCNAAAG | GAATGTTCTT | GGGTCCANT | CCCTCCTTTG | TTNCTTACGT | 660 |
| TGTNTTGGAC | CCNTGCTNGN | ATNACCCAAN | TGANATCCCC | NGAAGCACCC | TNCCCCTGGC | 720 |
| ATTTGANTTT | CNTAAATTCT | CTGCCCTACN | NCTGAAAGCA | CNATTCCCTN | GGCNCCNAAN | 780 |
| GGNGAACTCA | AGAAGGTCTN | NGAAAAACCA | CNCN | | | 814 |

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 760 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCATGCTGCT | CTTCCTCAAA | GTTGTTCTTG | TTGCCATAAC | AACCACCATA | GGTAAAGCGG | 60 |
| GCGCAGTGTT | CGCTGAAGGG | GTTGTAGTAC | CAGCGCGGGA | TGCTCTCCTT | GCAGAGTCCT | 120 |
| GTGTCTGGCA | GGTCCACGCA | ATGCCCTTTG | TCACTGGGGA | AATGGATGCG | CTGGAGCTCG | 180 |
| TCNAANCCAC | TCGTGTATTT | TTACANGCA | GCCTCCTCCG | AAGCNTCCGG | GCAGTTGGGG | 240 |
| GTGTCGTAC | ACTCCACTAA | ACTGTGATN | CANCAGCCCA | TTGCTGCAGC | GGAAGTGGGT | 300 |
| GGGCTGACAG | GTGCCAGAAC | ACACTGGATN | GGCCTTTCCA | TGGAAGGGCC | TGGGGGAAAT | 360 |
| CNCCTNANCC | CAAACTGCCT | CTCAAAGGCC | ACCTTGACAC | CCCCGACAGG | CTAGAAATGC | 420 |
| ACTCTTCTTC | CCAAAGGTAG | TTGTTCTTGT | TGCCCAAGCA | NCCTCCANCA | AACCAAAANC | 480 |
| TTGCAAAATC | TGCTCCGTGG | GGGTCAATNN | TACCANGGTT | GGGGAAANAA | ACCCGGCNGN | 540 |
| GANCCNCCTT | GTTTGAATGC | NAAGGNAATA | ATCCTCCTGT | CTTGCTTGGG | TGGAANAGCA | 600 |
| CAATTGAACT | GTTAACNTTG | GGCCGNGTTC | CNCTNGGGTG | GTCTGAAACT | AATCACCGTC | 660 |
| ACTGGAAAAA | GGTANGTGCC | TTCTTGAAT | TCCCAAANTT | CCCCTNGNTT | TGGGTNNTTT | 720 |
| CTCTCTNCC | CTAAAAATCG | TNTTCCCCC | CCNTANGGCG | | | 760 |

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTAAAAA CCCCCTCCAT TGAATGAAAA    60
CTTCCNAAAT TGTCCAACCC CCTCNNCCAA ATNNCCATTT CCGGGGGGGG GTTCCAAACC    120
CAAATTAATT TTGGANTTTA AATTAAATNT TNATTNGGGG AANAANCCAA ATGTNAAGAA    180
AATTTAACCC ATTATNAACT TAAATNCCTN GAAACCCNTG GNTTCCAAAA ATTTTTAACC    240
CTTAAATCCC TCCGAAATTG NTAANGGAAA ACCAAATTCN CCTAAGGCTN TTTGAAGGTT    300
NGATTTAAAC CCCCTTNANT TTTTTTNACC CNNGNCTNAA NTATTTNGNT TCCGGTGTTT    360
TCCTNTTAAN CNTNGGTAAC TCCCGNTAAT GAANNCCCT AANCCAATTA AACCGAATTT    420
TTTTTGAATT GGAAATTCCN NGGGAATTNA CCGGGGTTTT TCCCNTTTGG GGGCCATNCC    480
CCCNCTTTTCG GGGTTTGGGN NTAGGTTGAA TTTTNNANG NCCCCAAAAA NCCCCAANA    540
AAAAAACTCC CAAGNNTTAA TTNGAATNTC CCCCTCCCA GGCCTTTTGG GAAAGGNGGG    600
TTTNTGGGGG CCNGGGANTT CNTTCCCCCN TTNCNCCCC CCCCCCNGGT AAANGGTTAT    660
NGNNTTTGGT TTTTGGGCCC CTNANGGAC CTTCGGATN GAAATTAAAT CCCC GGNGC    720
GCCG                                     724

```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

TTTTTTTTTT TTTTCTTTG CTCACATTTA ATTTTATTT TGATTTTTTT TAATGCTGCA    60
CAACACAATA TTTATTTTCT TGTCTCTTT TATTTTATTT TATTTGTTTG CTGCTGCTGT    120
TTTATTTATT TTTACTGAAA GTGAGAGGGA ACTTTTGTGG CCTTTTTTCC TTTTCTGTA    180
GGCCGCCTTA AGCTTTCTAA ATTTGGAACA TCTAAGCAAG CTGAANGGAA AAGGGGGTTT    240
CGCAAAATCA CTCGGGGGAA NGGAAAGGTT GCTTTGTTAA TCATGCCCTA TGGTGGGTGA    300
TTAACTGCTT GTACAATTAC NTTTCACCTT TAATTAATTG TGCTNAANGC TTTAATTANA    360
CTTGGGGGTT CCTCCCCAN ACCAACCCCN CTGACAAAAA GTGCCNGCCC TCAAATNATG    420
TCCCGGCNNT CNTTGAAACA CACNGCNGAA NGTCTCTATT NTCCCNCCNC CAGGTNAAAA    480
TGAAGGGTTA CCATNTTTAA CNCCACCTCC ACNTGGCINN GCCTGAATCC TCNAAAANCN    540
CCCTCAANCN AATTNCTNNG CCCCAGTCNC GCNTNNGTCC CNCCCGGGCT CCGGGAANTN    600
CACCCCCNGA ANNCNNTNNC NAACNAAATT CCGAAAATAT TCCCNNTCNC TCAATTCCCC    660
CNNAGACTNT CCTCNCNAN CNCAATTTTC TTTTNTTCAC GAACNCGNNC CNNAATGN    720
NNNNCNCCTC CNCTNGTCCN NAATCNCCAN C                                     751

```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

GTGGTATTTT CTGTAAGATC AGGTGTTTCT CCCTCGTAGG TTAGAGGAA ACACCCCTCAT    60
AGATGAAAAC CCCCCGAGA CAGCAGCACT GCAACTGCCA AGCAGCCGGG GTAGGAGGGG    120
CGCCCTATGC ACAGCTGGGC CCTTGAGACA GCAGGGCTTC GATGTCAGGC TCGATGTCAA    180

```

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| TGGTCTGGAA | GCGGCGGCTG | TACCTGCGTA | GGGGCACACC | GTCAGGGCCC | ACCAGGAACT | 240 |
| TCTCAAAGTT | CCAGGCAACN | TCGTTGCGAC | ACACCGGAGA | CCAGGTGATN | AGCTTGGGGT | 300 |
| CGGTCATAAN | CGCGGTGGCG | TCGTGCTGG | GAGCTGGCAG | GGCCTCCCGC | AGGAAGGCNA | 360 |
| ATAAAAGGTG | CGCCCCGCA | CGTTCANCT | CGCACTTCTC | NAANACCATG | ANGTTGGGCT | 420 |
| CNAACCCACC | ACCANNCCGG | ACTTCCTTGA | NGGAATTCCC | AAATCTCTTC | GNTCTTGGGC | 480 |
| TTCTNCTGAT | GCCCTANCTG | GTTGCCCNEN | ATGCCAANCA | NCCCCAANCC | CCGGGGTCCCT | 540 |
| AAANCACCCN | CCTCCTCNTT | TCATCTGGGT | TNTTNTCCCC | GGACCNTGGT | TCCTCTCAAG | 600 |
| GGANCCCAT | TCTCNACCAN | TACTCACCNT | NCCCCCCNT | GNNACCCANC | CTTCTANNNG | 660 |
| TTCCCNCCCG | NCCTCTGGCC | CNTCAAANAN | GCTTNCACNA | CCTGGGTCTG | CCTTCCCCCC | 720 |
| TNCCCTATCT | GNACCCNCN | TTTGTCTCAN | TNT | | | 753 |

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| ACTATATCCA | TCACAACAGA | CATGCTTCAT | CCCATAGACT | TCTTGACATA | GCTTCAAATG | 60 |
| AGTGAACCCA | TCCTTGATT | ATATACATAT | ATGTTCTCAG | TATTTTGGGA | GCCTTTCCAC | 120 |
| TTCTTTAAAC | CTTGTTCAAT | ATGAACACTG | AAAATAGGAA | TTTGTGAAGA | GTTAAAAAGT | 180 |
| TATAGCTTGT | TTACGTAGTA | AGTTTTTGAA | GTCTACATTC | AATCCAGACA | CTTAGTTGAG | 240 |
| TGTTAAACTG | TGATTTTAA | AAAATATCAT | TTGAGAATAT | TCTTTCAGAG | GTATTTTCAT | 300 |
| TTTTACTTTT | TGATTAAATTG | TGTTTTATAT | ATTAGGGTAG | T | | 341 |

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTTACTGAA | TTTAGTTCTG | TGCTCTTCCT | TATTTAGTGT | TGTATCATAA | ATACTTTGAT | 60 |
| GTTTCAAACA | TTCTAAATAA | ATAATTTTCA | GTGGCTTCAT | A | | 101 |

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

| | |
|--|-----|
| ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCTTCCTG GTCCTCACCC | 60 |
| TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT | 120 |
| TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA | 180 |
| CCTCTTGAGA GGTCACTAAA GAGGACTTAA TATTTTCATAT CTACAAAATG ACCACAGGAT | 240 |
| TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC | 300 |
| TCGAA | 305 |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | |
|---|-----|
| ACATAAATAT CAGAGAAAAG TAGTCTTTGA AATATTTACG TCCAGGAGTT CTTTGTTTCT | 60 |
| GATTATTTGG TGTGTGTTTT GGTGTTGTGC CAAAGTATTG GCAGCTTCAG TTTTCATTTT | 120 |
| CTCTCCATCC TCGGGCATTG TTCCCAAATT TATATACCAG TCTTCGTCCA TCCACACGCT | 180 |
| CCAGAATTTT TCTTTGTAG TAATATCTCA TAGCTCGGCT GAGCTTTTCA TAGGTCATGC | 240 |
| TGCTGTTGTT CTCTTTTTTA CCCCATAGCT GAGCCACTGC CTCTGATTTC AAGAACCTGA | 300 |
| AGACGCCCTC AGATCGGTCT TCCCATTFTA TTAATCCTGG GTTCTTGCTT GGGTTCAAGA | 360 |
| GGATGTCGCG GATGAATTCC CATAAGTGAG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC | 420 |
| ACTTGGCAGG GGGGTCTTGC TCCTTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC | 480 |
| TGGTGGTTGT CATGGAGATC TGAGCCCGGC AGAAAGTTTT GCTGTCCAAC AAATCTACTG | 540 |
| TGCTACCATA GTTGGTGTC TATAAATAGT TCTNGTCTTT CCAGGTGTTC ATGATGGAAG | 600 |
| GCTCAGTTTG TTCAGTCTTG ACAATGACAT TGTGTGTGGA CTGGAACAGG TCACTACTGC | 660 |
| ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCC GCCGTCCCTG | 720 |
| CCGCCCCGGT GAACTCCTGC AAACATCATG TGCAAAGGTG CTCGCCGTG ATGTCGAAC | 780 |
| CNTGGAAAGG GATACAATTG GCATCCAGCT GGTGTTGTG CAGGAGGTGA TGGAGCCACT | 840 |
| CCCACACCTG GT | 852 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

| | |
|---|-----|
| ACAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG | 60 |
| AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTGCGAGTG CCCTACCGCG GGGAACTCTT | 120 |
| GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCGAGTGC | 180 |

TGAACGTGTC GGTGGTGTCT GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT

234

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

| | |
|---|-----|
| ACTTTTTATT TAAATGTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAC ATGGTGTGTA | 60 |
| ATTGATAGC AATATTTTGG AGATTACAGA GTTTTAGTAA TTACCAATTA CACAGTTAAA | 120 |
| AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAAA | 180 |
| TGANTATAAC TAATTGACAA TGGAAAATCA ATTTTAATGT GAATTGCACA TTATCCTTTA | 240 |
| AAAGCTTTCA AAANAAANAA TTATTGCAGT CTANTTAATT CAAACAGTGT TAAATGGTAT | 300 |
| CAGGATAAAN AACTGAAGGG CANAAAGAAT TAATTTTCAC TTCATGTAAC NCACCCANAT | 360 |
| TTACAATGGC TTAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCCTTC | 420 |
| TGGTCTCTAA TCTGCCCTAC TCTTTGGGTG TGGCTTTGAT CCTCTGGAGA CAGCTGCCAG | 480 |
| GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT | 540 |
| GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT | 590 |

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

| | |
|--|-----|
| ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTTAAAG AAGGAAAAAA AACGAGGCCC | 60 |
| TGAACAGAAT TTTCCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGGA GGTTCAGAC | 120 |
| GCTTCACTGC TTGAAACTTA AATGGATGTG GGACANAATT TTCTGTAATG ACCCTGAGGG | 180 |
| CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCCAA | 240 |
| AACATCAAAG AAAGGAAGGT GGCCTCATACT CTTCCAGCCT ACACAGTTCT CCAGGGCTCT | 300 |
| CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCCCAGG CTCCTGTGTG | 360 |
| CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCACC CTCTGCTGAT CTGCGTGGC | 420 |
| CCACACTCCT TGAACACACA TCCCAGGTT ATATTCTTGG ACATGGCTGA ACCTCCTATT | 480 |
| CCTACTTCCG AGATGCCTTG CTCCCTGCAG CCTGTCAAAA TCCCCTCAC CCTCCAAACC | 540 |
| ACGGCATGGG AAGCCTTTCT GACTTGCCTG ATTACTCCAG CATCTTGGA CAATCCCTGA | 600 |
| TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC | 660 |
| AGGCTGCTGG CTTCAAATTN TGGCTCATTT ACGAGCTATG GGACCTGGG CAAGTNATCT | 720 |
| TCACTTCTAT GGGCNTCATT TTGTTCTACC TGCAAAATGG GGGATAATAA TAGT | 774 |

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

| | |
|--|-----|
| CANAAATTGA AATTTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATTT | 60 |
| TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTTCCTT AATTACAGCT CAACGCAACT | 120 |
| TGGT | 124 |

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

| | |
|--|-----|
| GCCGATGCTA CTATTTTATT GCAGGAGGTG GGGGTGTTT TATTATTCTC TCAACAGCTT | 60 |
| TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAT | 120 |
| TTAGGGCACC CATATCCCA GCANTGT | 147 |

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

| | |
|---|-----|
| ACATTAAATT AATAAAAGGA CTGTTGGGGT TCTGCTAAAA CACATGGCTT GATATATTGC | 60 |
| ATGGTTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT | 107 |

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

| | |
|--|-----|
| GTCCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGACACGG | 60 |
| CGGGAAGGAA AGGCAGAGAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG | 120 |
| GCCTTGCAAG GTCAGAAAGG GGA CTCAGG CTTCCACCAC AGCCCTGCCC CACTTGGCCA | 180 |
| CCTCCCTTTT GGGACCAGCA ATGT | 204 |

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

| | |
|--|-----|
| ACAAAGATAA CATTTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGTA | 60 |
| GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTAAAA AGTTAGAAAT GTATAAAACA | 120 |
| CCATCAGACA GGTTTTTTAAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA | 180 |
| AAAACCTTCT GTATCAATTT CTTTGTTC AATGACTGA CTTAANTATT TTAAATATT | 240 |
| TCANAAACAC TTCCTCAAAA ATTTTCAANA TGGTAGCTTT CANATGTNCC CTCAGTCCCA | 300 |
| ATGTTGCTCA GATAATAAAA TCTCGTGAGA ACTTACCACC CACCACAAGC TTTCTGGGGC | 360 |
| ATGCAACAGT GTCTTTTCTT TNCTTTTCT TTTTTTTTT TTACAGGCAC AGAAACTCAT | 420 |
| CAATTTTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT | 480 |
| ATCACTCTTG T | 491 |

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

| | |
|---|-----|
| ACATAATTTA GCAGGGCTAA TTACCATAAG ATGCTATTTA TTAANAGGTN TATGATCTGA | 60 |
| GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCAGCAT TTTCTTTTGT CTTTGATAAC | 120 |
| ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAAA GTTCAGAAAC ATTAGCTGCT | 180 |
| CAATCAAATC TCTACATAAC ACTATAGTAA TTAACAGTT AAAAAAAGT GTTGAAATCT | 240 |
| GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAAANC | 300 |
| AGCTTTGANT TTCTTTGTGC TGATANGAGG AAAGGCTGAA TTACCTTGTT GCCTCTCCCT | 360 |
| AATGATTGGC AGGTCNGGTA AATNCCAAAA CATATTCCAA CTCAACACTT CTTTTCNCG | 420 |
| TANCTTGANT CTGTGTATTC CAGGANCAGG CGGATGGAAT GGGCCAGCCC NCGGATGTTC | 480 |
| CANT | 484 |

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
ACTAAACCTC GTGCTTGTGA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG      60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTTGG CACTGGCTAG      120
TCTATGTCCT CTCAAGTGCC TTTTGTGTTG T                                151
```

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
ACCTGGCTTG TCTCCGGGTG GTTCCCGGCG CCCCCACGG TCCCCAGAAC GGACACTTTC      60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T                                91
```

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTTAT GTAAGGGACT TGAGTATACT      60
TGGATTTTTG GTATCTGTGG GTTGGGGGGA CGGTCCAGGA ACCAATACCC CATGGATACC      120
AAGGGACAAC TGT                                133
```

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

| | |
|---|-----|
| ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC | 60 |
| GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA | 120 |
| TCTCANTGGG CTGGATNCAT GCAGGGT | 147 |

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

| | |
|--|-----|
| ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGTAATAAC ATTGAATTTT CTGTATACTC | 60 |
| TGATTACATA CATTTATCCT TAAAAAAGA TGTAATCTT AATTTTATG CCATCTATTA | 120 |
| ATTTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TTAAC TAGTT | 180 |
| TTGACTTCTA AGTTTGGT | 198 |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

| | |
|---|-----|
| ACAACAAATG GGTGTGAGG AAGTCTTATC AGCAAACTG GTGATGGCTA CTGAAAAGAT | 60 |
| CCATTGAAAA TTATCATTAA TGATTTTAAA TGACAACTTA TCAAAAATC ACTCAATTTT | 120 |
| CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA | 180 |
| TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG | 240 |
| CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT | 300 |
| TTTCGTCTTT ATTGGACTTC TTTGAAGAGT | 330 |

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

| | |
|---|-----|
| ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC | 60 |
| GTCGTGGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC | 120 |
| TCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGCG ATTCCCGTGC CTGGT | 175 |

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

| | |
|---|-----|
| ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT | 60 |
| GTTTGTGCT CTTCAACAGT ATCCTCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC | 120 |
| TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT | 154 |

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

| | |
|----------------------------------|----|
| CGCTCGAGCC CTATAGTGAG TCGTATTAGA | 30 |
|----------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

| | |
|--|----|
| ACAAGTCATT TCAGCACCCT TTGCTCTTCA AAAGTACCA TCTTTTATAT TTAATGCTTC | 60 |
| CTGTATGAAT AAAAATGGTT ATGTCAAGT | 89 |

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

| | |
|--|----|
| ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAATAAA GGTTCCTGCAG | 60 |
| AATCAGTGCA TCCAGGATTG GTCCTTGAT CTGGGGT | 97 |

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

| | |
|---|-----|
| ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCT TTGATGGCA | 60 |
| GCATGGCGTC CTAGGCCTTG ACACAGCGGC TGGGTTTGG GCTNTCCCA ACCGCACACC | 120 |
| CCAACCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT | 180 |
| TCGGTCATAA NATGAAATCC CAANGGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA | 240 |
| GGTGCTGTTT GCTCAGCCAG AAAACAGCTG CCTGGCATTG GCCGCTGAAC TATGAACCCG | 300 |
| TGGGGGTGAA CTACCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG | 360 |
| GGGCGGGAGG AGCATGT | 377 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

| | |
|---|-----|
| ACGCCTTTCC CTCAGAATTC AGGGAAGAGA CTGTCGCCTG CCTTCCTCCG TTGTTGCGTG | 60 |
| AGAACCCGTG TGCCCCCTTC CACCATATCC ACCCTCGCTC CATCTTTGAA CTCAAACACG | 120 |
| AGGAACTAAC TGCACCCTGG TCCTCTCCCC AGTCCCCAGT TCACCCTCCA TCCCTCACCT | 180 |
| TCCTCCACTC TAAGGGATAT CAACACTGCC CAGCACAGGG GCCCTGAATT TATGTGGTTT | 240 |
| TTATATATTT TTTAATAAGA TGCACCTTAT GTCATTTTTT AATAAAGTCT GAAGAATTAC | 300 |
| TGTTT | 305 |

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

| | |
|--|-----|
| ACTACACACA CTCCACTTGC CCTTGTGAGA CACTTTGTCC CAGCACTTTA GGAATGCTGA | 60 |
| GGTCGGACCA GCCACATCTC ATGTGCAAGA TTGCCCAGCA GACATCAGGT CTGAGAGTTC | 120 |
| CCCTTTTAAA AAAGGGGACT TGCTTAAAAA AGAAGTCTAG CCACGATTGT GTAGAGCAGC | 180 |
| TGTGCTGTGC TGGAGATTCA CTTTGTGAGAG AGTTCTCCTC TGAGACCTGA TCTTTAGAGG | 240 |
| CTGGGCAGTC TTGCACATGA GATGGGGCTG GTCTGATCTC AGCACTCCTT AGTCTGCTTG | 300 |
| CCTCTCCAG GGCCCCAGCC TGGCCACACC TGCTTACAGG GCACTCTCAG ATGCCCATAC | 360 |
| CATAGTTTCT GTGCTAGTGG ACCGT | 385 |

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

| | |
|---|----|
| ACTTAACCAG ATATATTTTT ACCCCAGATG GGGATATTCT TTGTAAAAAA TGAAAATAAA | 60 |
| GTTTTTTTAA TGG | 73 |

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTAGTCCAG | TGTGGTGGAA | TTCCATTGTG | TTGGGGGCTC | TCACCCTCCT | CTCCTGCAGC | 60 |
| TCCAGCTTTG | TGCTCTGCCT | CTGAGGAGAC | CATGGCCCAG | CATCTGAGTA | CCCTGCTGCT | 120 |
| CCTGCTGGCC | ACCCTAGCTG | TGGCCCTGGC | CTGGAGCCCC | AAGGAGGAGG | ATAGGATAAT | 180 |
| CCCGGGTGGC | ATCTATAACG | CAGACCTCAA | TGATGAGTGG | GTACAGCGTG | CCCTTCACTT | 240 |
| CGCCATCAGC | GAGTATAACA | AGGCCACCAA | AGATGACTAC | TACAGACGTC | CGCTGCGGGT | 300 |
| ACTAAGAGCC | AGGCAACAGA | CCGTTGGGGG | GGTGAATTAC | TTCTTCGACG | TAGAGGTGGG | 360 |
| CCGAACCATA | TGTACCAAGT | CCCAGCCCAA | CTTGGACACC | TGTGCCTTCC | ATGAACAGCC | 420 |
| AGAACTGCAG | AAGAAACAGT | TGTGCTCTTT | CGAGATCTAC | GAAGTTCCTT | GGGGAGAACA | 480 |
| GAANGTCCCT | GGGTGAAATC | CAGGTGTCAA | GAAATCCTAN | GGATCTGTTG | CCAGGC | 536 |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| ATGACCCCTA | ACAGGGGCCC | TCTCAGCCCT | CCTAATGACC | TCCGGCCTAG | CCATGTGATT | 60 |
| TCACTTCCAC | TCCATAACGC | TCCTCATACT | AGGCCTACTA | ACCAACACAC | TAACCATATA | 120 |
| CCAATGATGG | CGCGATGTAA | CACGAGAAAG | CACATACCAA | GGCCACCACA | CACCACCTGT | 180 |
| CCAAAAAGGC | CTTCGATACG | GGATAATCCT | ATTTATTACC | TCAGAAGTTT | TTTTCTTCGC | 240 |
| AGGGATTTT | CTGAGCCTTT | TACCACTCCA | GCCTAGCCCC | TACCCCCCAA | CTAGGAGGGC | 300 |
| ACTGGCCCCC | AACAGGCATC | ACCCCGCTAA | ATCCCCTAGA | AGTCCCCTC | CTAAACACAT | 360 |
| CCGTATTACT | CGCATCAGGA | GTATCAATCA | CCTGAGCTCA | CCATAGTCTA | ATAGAAAAACA | 420 |
| ACCGAAACCA | AATTATTCAA | AGCACTGCTT | ATTACAATTT | TACTGGGTCT | CTATTTT | 477 |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

| | | | | | | |
|------------|-------------|------------|-------------|------------|------------|-----|
| AGAGCTATAG | GTACAGTGTG | ATCTCAGCTT | TGCAAAACACA | TTTTCTACAT | AGATAGTACT | 60 |
| AGGTATTAAT | AGATATGTAA | AGAAAGAAAT | CACACCATTA | ATAATGGTAA | GATTGGTTTA | 120 |
| TGTGATTTTA | GTGGTATTTT | TGGCACCCTT | ATATATGTTT | TCCAAACTTT | CAGCAGTGAT | 180 |
| ATTATTTCCA | TAACTTAAAA | AGTGAGTTTG | AAAAAGAAAA | TCTCCAGCAA | GCATCTCATT | 240 |
| TAAATAAAGG | TTTGTCTATCT | TTAAAAATAC | AGCAATATGT | GACTTTTAA | AAAAGCTGTC | 300 |
| AAATAGGTGT | GACCCTACTA | ATAATTATTA | GAAATACATT | TAAAAACATC | GAGTACCTCA | 360 |
| AGTCAGTTTG | CCTTGAAAAA | TATCAAATAT | AACTCTTAGA | GAAATGTACA | TAAAAGAATG | 420 |
| CTTCGTAATT | TTGGAGTANG | AGGTTCCTCT | CTCAATTTTG | TATTTTAAA | AAGTACATGG | 480 |

TAAAAAAAAA AATTCACAAC AGTATATAAG GCTGTAAAAT GAAGAATTCT GCC

533

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 511 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

| | |
|--|-----|
| TATTACGGAA AAACACACCA CATAATTCAA CTANCAAAGA ANACTGCTTC AGGGCGTGTA | 60 |
| AAATGAAAGG CTTCCAGGCA GTTATCTGAT TAAAGAACAC TAAAAGAGGG ACAAGGCTAA | 120 |
| AAGCCGCAGG ATGTCTACAC TATANCAGGC GCTATTTGGG TTGGCTGGAG GAGCTGTGGA | 180 |
| AAACATGGAN AGATTGGTGC TGGANATCGC CGTGGCTATT CCTCATGTGTT ATTACANAGT | 240 |
| GAGGTTCTCT GTGTGCCAC TGGTTTGAAA ACCGTTCTNC AATAATGATA GAATAGTACA | 300 |
| CACATGAGAA CTGAAATGGC CCAAACCCAG AAAGAAAGCC CAACTAGATC CTCAGAAAC | 360 |
| GCTTCTAGGG ACAATAACCG ATGAAGAAAA GATGGCCTCC TTGTGCCCC GTCTGTTATG | 420 |
| ATTTCTCTCC ATTGCAGCNA NAAACCCGTT CTTCTAAGCA AACNCAGGTG ATGATGGCNA | 480 |
| AAATACACCC CCTCTTGAAG NACCNGGAGG A | 511 |

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

| | |
|---|-----|
| CAGTGCCAGC ACTGGTGCCA GTACCAGTAC CAATAACAGT GCCAGTGCCA GTGCCAGCAC | 60 |
| CAGTGGTGGC TTCAGTGCTG GTGCCAGCCT GACCGCCACT CTCACATTTG GGCTCTTCGC | 120 |
| TGGCCTTGGT GGAGCTGGTG CCAGCACCAG TGGCAGCTCT GGTGCCTGTG GTTTCTCCTA | 180 |
| CAAGTGAGAT TTAGATATT GTTAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC | 240 |
| CTCAGAAACC TACTCAACAC AGCACTCTAG GCAGCCACTA TCAATCAATT GAAGTTGACA | 300 |
| CTCTGCATTA AATCTATTTG CCATTCTGA AAAAAAAAAA AAAAAAAGGG CGGCCGCTCG | 360 |
| ANTCTAGAGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT ANTGGCCAGC | 420 |
| CATCTGTTGT TTGCCCTCC CCCGNTGCCT TCCTTGACCC TGGAAAGTGC CACTCCCACT | 480 |
| GTCTTTTCT AANTAAAT | 499 |

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

| | |
|---|-----|
| TTTCATAGGA GAACACACTG AGGAGATACT TGAAGAATTT GGATTCAGCC GCGAAGAGAT | 60 |
| TTATCAGCTT AACTCAGATA AAATCATTGA AAGTAATAAG GTAAAAGCTA GTCTCTAACT | 120 |
| TCCAGGCCCA CGGCTCAAGT GAATTTGAAT ACTGCATTTA CAGTGTAGAG TAACACATAA | 180 |
| CATTGTATGC ATGGAAACAT GGAGGAACAG TATTACAGTG TCCTACCACT CTAATCAAGA | 240 |
| AAAGAATTAC AGACTCTGAT TCTACAGTGA TGATTGAATT CTAAAAATGG TAATCATTAG | 300 |
| GGCTTTTGAT TTATAANACT TTGGGTACTT ATACTAAATT ATGGTAGTTA TACTGCCTTC | 360 |
| CAGTTTGCTT GATATATTG TTGATATTAA GATTCTTGAC TTATATTTTG AATGGGTTCT | 420 |
| ACTGAAAAAN GAATGATATA TTCTTGAAGA CATCGATATA CATTTATTTA CACTCTTGAT | 480 |
| TCTACAATGT AGAAAATGAA GGAAATGCCC CAAATTGTAT GGTGATAAAA GTCCCGT | 537 |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

| | |
|---|-----|
| CAAANACAAT TGTTCAAAAG ATGCAAATGA TACACTACTG CTGCAGCTCA CAAACACCTC | 60 |
| TGCATATTAC ACGTACCTCC TCCTGCTCCT CAAGTAGTGT GGTCTATTTT GCCATCATCA | 120 |
| CCTGCTGTCT GCTTAGAAGA ACGGCTTTCT GCTGCAANGG AGAGAAATCA TAACAGACGG | 180 |
| TGGCACAAGG AGGCCATCTT TTCTCATCG GTTATGTGCC CTAGAAGCGT CTTCTGAGGA | 240 |
| TCTAGTTGGG CTTTCTTTCT GGGTTTGGGC CATTTCANTT CTCATGTGTG TACTATTCTA | 300 |
| TCATTATTGT ATAACGGTTT TCAAACNGT GGGCACNCAG AGAACCTCAC TCTGTAATAA | 360 |
| CAATGAGGAA TAGCCACGGT GATCTCCAGC ACCAAATCTC TCCATGTTNT TCCAGAGCTC | 420 |
| CTCCAGCCAA CCCAAATAGC CGCTGCTATN GTGTAGAACA TCCCTGN | 467 |

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

| | |
|---|-----|
| AAGCTGACAG CATTGCGGCC GAGATGTCTC GTCCTGTGGC CTTAGCTGTG CTCGCGCTAC | 60 |
| TCTCTCTTTT TGGCCTGGAG GCTATCCAGC GTACTCCAAA GATTGAGGTT TACTCACGTC | 120 |
| ATCCAGCAGA GAATGGAAAG TCAAATTTCC TGAATTGCTA TGTGTCTGGG TTTCATCCAT | 180 |
| CCGACATTGA AGTTGACTTA CTGAAGAATG GAGAGAGAAT TGAAAAAGTG GAGCATTGAG | 240 |
| ACTTGTCTTT CAGCAAGGAC TGGTCTTTCT ATCTCTTGTA CTACACTGAA TTCACCCCCA | 300 |
| CTGAAAAAGA TGAGTATGCC TGCCGTGTGA ACCATGTGAC TTTGTCACAG CCCAAGATNG | 360 |

TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT

400

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

| | |
|--|-----|
| CTGGAGTGCC TTGGTGTTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT | 60 |
| CCAGCTGCCC CGGCGGGGGA TGCGAGGCTC GGAGCACCCT TGCCCGGCTG TGATTGCTGC | 120 |
| CAGGCACTGT TCATCTCAGC TTTTCTGTCC CTTTGCTCCC GGCAAGCGCT TCTGCTGAAA | 180 |
| GTTTCATATCT GGAGCCTGAT GTCTTAACGA ATAAAGGTCC CATGCTCCAC CCGAAAAAAA | 240 |
| AAAAAAA | 248 |

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

| | |
|---|-----|
| ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCCAA CACAATGGCT ACCTTTAACA | 60 |
| TCACCCAGAC CCCGCCCTGC CCGTGCCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC | 120 |
| TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTTT ATAAATGCCT | 180 |
| GATTTAAAAA AAAAAAAAAA A | 201 |

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 552 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

| | |
|--|-----|
| TCCTTTTGTG AGGTTTTTGA GACAACCCTA GACCTAAACT GTGTCACAGA CTTCTGAATG | 60 |
| TTTAGGCAGT GCTAGTAATT TCCTCGTAAT GATTCTGTTA TTA CTTTCTT ATTCTTTATT | 120 |
| CCTCTTTCTT CTGAAGATTA ATGAAGTTGA AAATTGAGGT GGATAAATAC AAAAAGGTAG | 180 |

| | |
|---|-----|
| TGTGATAGTA TAAGTATCTA AGTGCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT | 240 |
| ATGCAAGTTA GTAATTACTC AGGGTTAACT AAATTACTTT AATATGCTGT TGAACCTACT | 300 |
| CTGTTCCCTTG GCTAGAAAAA ATTATAAACA GGACTTTGTT AGTTGGGAA GCCAAATTGA | 360 |
| TAATATTCTA TGTCTAAAA GTTGGGCTAT ACATAAANTA TNAAGAAATA TGGAAATTTTA | 420 |
| TTCACAGGAA TATGGGGTTC ATTTATGAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC | 480 |
| CNGTTTTGGT TAATACGTTA ATATGTCCTN AATNAACAAG GCNTGACTTA TTTCCAAAAA | 540 |
| AAAAAAAAAA AA | 552 |

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

| | |
|--|-----|
| ACAGGGATTG GAGATGCTAA GGCCCCAGAG ATCGTTTGAT CCAACCCTCT TATTTTCAGA | 60 |
| GGGGAAAATG GGGCCTAGAA GTTACAGAGC ATCTAGCTGG TGCGCTGGCA CCCCTGGCCT | 120 |
| CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT | 180 |
| GCAATTCACG TTGCCACCTC CAACTTAAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA | 240 |
| AGGTTAAACT TTCCACCCCA GAAAAGGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC | 300 |
| TCTTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCCTCCTT GGGGGTTGAT AGGAANTNTC | 360 |
| TCTTGGCTTT TCTCAATAAAA TCTCTATCCA TCTCATGTTT AATTGTTGAC GCNTAAAAAT | 420 |
| GCTGAAAAAA TTAAATGTT CTGGTTTCNC TTTAAAAAAA AAAAAAAAAA AAAAAA | 476 |

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

| | |
|---|-----|
| TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCTGGA GGAGCCCAGT | 60 |
| TTCTTCTGTA TCTTTCTTTT CTGGGGGATC TTCCTGGCTC TGCCCCCTCA TTCCCAGCCT | 120 |
| CTCATCCCCA TCTTGCACTT TTGCTAGGGT TGGAGGCGCT TTCCTGGTAG CCCCTCAGAG | 180 |
| ACTCAGTCAG CGGGAATAAG TCCTAGGGGT GGGGGGTGTG GCAAGCCGGC CT | 232 |

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

| | |
|---|-----|
| AGGCGGGAGC AGAAGCTAAA GCCAAAGCCC AAGAAGAGTG GCAGTGCCAG CACTGGTGCC | 60 |
| AGTACCAGTA CCAATAACAT GCCAGTGCCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG | 120 |
| GTGCCAGCCT GACCGCCACT CTCACATTG GGCTCTTCGC TGGCCTTGGT GGAGCTGGTG | 180 |
| CCAGCACCAG TGGCAGCTCT GGTGCCTGTG GTTTCTCCTA CAAGTGAGAT TTAGATATT | 240 |
| GTTAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC CTCAGAAACC TACTCAACAC | 300 |
| AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTTG | 360 |
| CCATTTCAAA AAAAAAAAAA AAA | 383 |

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

| | |
|---|-----|
| ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA | 60 |
| GGGAGATCGA GTCTATACGC TGAAGAAATT TGACCCGATG GGACAACAGA CCTGCTCAGC | 120 |
| CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA | 180 |
| ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG | 240 |
| ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TCGGACTGTG | 300 |
| AGCCCTGATG CCTTTTTGCC AGCCATACTC TTTGGCNTCC AGTCTCTCGT GGCGATTGAT | 360 |
| TATGCTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGAACACAT TTGANTTTT | 420 |
| TTTCNCATAT TTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA | 480 |
| AAAAAAAAA AAAA | 494 |

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

| | |
|---|-----|
| GCTGGTAGCC TATGGCGTGG CCACGGANGG GCTCCTGAGG CACGGGACAG TGAATTCCCA | 60 |
| AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGGCA GATTCCCCAG | 120 |
| GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG | 180 |
| GCACACCTC CTGGGGCCCA GCGGGGCACC TGCGTCTCCC AGTATGCCAA CTGGCTGGTG | 240 |
| GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG | 300 |
| CCATGTTTCA TTACACATTG GGCAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC | 360 |
| AGCGTTNCCG CCTCATCCGG | 380 |

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

GAGTTAGCTC CTCCACAACC TTGATGAGGT CGTCTGCAGT GGCCTCTCGC TTCATACCGC      60
TNCCATCGTC ATACTGTAGG TTTGCCACCA CCTCCTGCAT CTTGGGGCGG CTAATATCCA      120
GGAAACTCTC AATCAAGTCA CCGTCNATNA AACCTGTGGC TGGTTCTGTC TTCCGCTCGG      180
TGTGAAAGGA TCTCCAGAAG GAGTGCTCGA TCTTCCCCAC ACTTTTGATG ACTTTATTGA      240
GTCGATTCTG CATGTCCAGC AGGAGGTTGT ACCAGCTCTC TGACAGTGAG GTCACCAGCC      300
CTATCATGCC NTTGAACGTG CCGAAGAACA CCGAGCCTTG TGTGGGGGGT GNAGTCTCAC      360
CCAGATTCTG CATTACCAGA NAGCCGTGGC AAAAGANATT GACAACTCGC CCAGGNNGAA      420
AAAGAACACC TCCTGGAAGT GCTNGCCGCT CCTCGTCCNT TGGTGGNNGC GCNTNCCTTT      480
T

```

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

AACATCTTCC TGTATAATGC TGTGTAATAT CGATCCGATN TTGTCTGCTG AGAATTCATT      60
ACTTGGAATA GCAACTTNAA GCCTGGACAC TGGTATTAAA ATTCACAATA TGCAACACTT      120
TAAACAGTGT GTCAATCTGC TCCCTTACTT TGTCAACACC AGTCTGGGAA TAAGGGTATG      180
CCCTATTACAC ACCTGTTAAA AGGGCGCTAA GCATTTTTGA TTCAACATCT TTTTTTTTGA      240
CACAAGTCCG AAAAAAGCAA AAGTAAACAG TTNTTAATTT GTTAGCCAAT TCACTTTCTT      300
CATGGGACAG AGCCATTTGA TTTAAAAAGC AAATTGCATA ATATTGAGCT TTGGGAGCTG      360
ATATNTGAGC GGAAGANTAG CCTTTCTACT TCACCAGACA CAACTCCTTT CATATTGGGA      420
TGTTNACNAA AGTTATGTCT CTTACAGATG GGATGCTTTT GTGGCAATTC TG          472

```

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| AGAAACCACT | ATCTCTNAAA | ACAACCTCTC | ATACCTTGTTG | GACCTAATTT | TGTGTGCGTG | 60 |
| TGTGTGTGCG | CGCATATTAT | ATAGACAGGC | ACATCTTTTT | TACTTTTGTA | AAAGCTTATG | 120 |
| CCTCTTTGGT | ATCTATATCT | GTGAAAGTTT | TAATGATCTG | CCATAATGTC | TTGGGGACCT | 180 |
| TTGTCTTCTG | TGTAAATGGT | ACTAGAGAAA | ACACCTATNT | TATGAGTCAA | TCTAGTTNGT | 240 |
| TTTATTCGAC | ATGAAGGAAA | TTTCCAGATN | ACAACACTNA | CAAACCTCTC | CTTGACTAGG | 300 |
| GGGGACAAAG | AAAAGCANAA | CTGAACATNA | GAAACAATTN | CCTGGTGAGA | AATTNCATAA | 360 |
| ACAGAAATTG | GGTNGTATAT | TGAAANANNG | CATCATTNAA | ACGTTTTTTT | TTT | 413 |

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGCAGCGGGT | CCTCTCTATC | TAGCTCCAGC | CTCTCGCCTG | CCCCACTCCC | CGCGTCCCCG | 60 |
| GTCCTAGCCN | ACCATGGCCG | GGCCCCCTGC | CGCCCCGCTG | CTCCTGCTGG | CCATCCTGGC | 120 |
| CGTGGCCCTG | GCCGTGAGCC | CCGCGGCCGG | CTCCAGTCCC | GGCAAGCCGC | CGCGCCTGGT | 180 |
| GGGAGGCCCA | TGGACCCCGC | GTGGAAGAAG | AAGGTGTGCG | GCGTGCACTG | GACTTTGCCG | 240 |
| TCGGCNANTA | CAACAAACCC | GCAACNACTT | TTACCNAGCN | CGCGCTGCAG | GTTGTGCCGC | 300 |
| CCCAANCAAA | TTGTTACTNG | GGGTAANTAA | TTCTTGGAAG | TTGAACCTGG | GCCAAACNNG | 360 |
| TTTACCAGAA | CCNAGCCAAT | TNGAACAATT | NCCCCTCCAT | AACAGCCCCT | TTTAAAAAGG | 420 |
| GAANCANTCC | TGNTCTTTTC | CAAATTTT | | | | 448 |

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GAATTTTGTG | CACTGGCCAC | TGTGATGGAA | CCATTGGGCC | AGGATGCTTT | GAGTTTATCA | 60 |
| GTAGTGATTC | TGCCAAAGTT | GGTGTGTGAA | CATGAGTATG | TAAAATGTCA | AAAAATTAGC | 120 |
| AGAGGTCTAG | GTCTGCATAT | CAGCAGACAG | TTTGTCCGTG | TATTTTGTAG | CCTTGAAGTT | 180 |
| CTCAGTGACA | AGTTNNTTCT | GATGCGAAGT | TCTNATTCCA | GTGTTTTAGT | CCTTTGCATC | 240 |
| TTTATGTGTT | AGACTTGCCCT | CTNTNAAATT | GCTTTTGTNT | TCTGCAGGTA | CTATCTGTGG | 300 |
| TTTAACAAAA | TAGAANNACT | TCTCTGCTTN | GAANATTGTA | ATATCTTACA | TCTNAAAATN | 360 |
| AATTCTCTCC | CCATANNAAA | ACCCANGCCC | TTGGGANAAT | TTGAAAAANG | GNTCCTTCNN | 420 |
| AATTCNNANA | ANTTCAGNTN | TCATACAACA | NAACNGGAN | CCC | | 463 |

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

| | |
|--|-----|
| AGGGATTGAA GGTCTNTTNT ACTGTCGGAC TGTTCANCCA CCAACTCTAC AAGTTGCTGT | 60 |
| CTTCCACTCA CTGTCTGTAA GCNTNTTAAAC CCAGACTGTA TCTTCATAAA TAGAACAAAT | 120 |
| TCTTCACCAG TCACATCTTC TAGGACCTTT TTGGATTGAG TTAGTATAAG CTCTTCCACT | 180 |
| TCCTTTGTGA AGACTTCATC TGGTAAAGTC TTAAGTTTTG TAGAAAGGAA TTTAATTGCT | 240 |
| CGTTCTCTAA CAATGTCCTC TCCTTGAAGT ATTTGGCTGA ACAACCCACC TNAAGTCCCT | 300 |
| TTGTGCATCC ATTTTAAATA TACTTAATAG GGCATTGGTN CACTAGGTTA AATTCTGCAA | 360 |
| GAGTCATCTG TCTGCAAAAG TTGCGTTAGT ATATCTGCCA | 400 |

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

| | |
|--|-----|
| GAGCTCGGAT CCAATAATCT TTGTCTGAGG GCAGCACACA TATNCAGTGC CATGGNAACT | 60 |
| GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCATTCCC TGAGTCAGAC | 120 |
| ATGCCTCTTT GACTACCGTG TGCCAGTGCT GGTGATTCTC ACACACCTCC NNCCGCTCTT | 180 |
| TGTGGAAAAA CTGGCACTTG NCTGGAAC TA GCAAGACATC ACTTACAAAT TCACCCACGA | 240 |
| GACACTTGAA AGGTGTAACA AAGCGACTCT TGCATTGCTT TTTGTCCCTC CGGCACCACT | 300 |
| TGTCAATACT AACCCGCTGG TTTGCCTCCA TCACATTTGT GATCTGTAGC TCTGGATACA | 360 |
| TCTCCTGACA GTACTGAAGA ACTTCTTCTT TTGTTTCAAA AGCAACTCTT GGTGCCTGTT | 420 |
| NGATCAGGTT CCCATTTCCC AGTCCGAATG TTCACATGGC ATATNTTACT TCCCACAAAA | 480 |

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| ATACAGCCCA | NATCCACCA | CGAAGATGCG | CTTGTTGACT | GAGAACCTGA | TGCGGTCACT | 60 |
| GGTCCCGCTG | TAGCCCCAGC | GACTCTCCAC | CTGCTGGAAG | CGGTTGATGC | TGCACTCCTT | 120 |
| CCCACGCAGG | CAGCAGCGGG | GCCGGTCAAT | GAAGTCCACT | CGTGGCTTGG | GGTTGACGGT | 180 |
| TAANTGCAGG | AAGAGGCTGA | CCACCTCGCG | GTCCACCAGG | ATGCCCCGACT | GTGCGGGACC | 240 |
| TGCAGCGAAA | CTCCTCGATG | GTCATGAGCG | GGAAGCGAAT | GANGCCCAGG | GCCTTGCCCA | 300 |
| GAACCTTCCG | CCTGTTCTCT | GGCGTCACCT | GCAGCTGCTG | CCGCTNACAC | TCGGCCTCGG | 360 |
| ACCAGCGGAC | AAACGGCGTT | GAACAGCCGC | ACCTCACGGA | TGCCCANTGT | GTCGCGCTCC | 420 |
| AGGAACGGCN | CCAGCGTGTC | CAGGTCAATG | TCGGTGAANC | CTCCGCGGGT | AATGGCG | 477 |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GAACGGCTGG | ACCTTGCTC | GCATTGTGCT | GCTGGCAGGA | ATACCTTGGC | AAGCAGCTCC | 60 |
| AGTCCGAGCA | GCCCCAGACC | GCTGCCGCC | GAAGCTAAGC | CTGCCTCTGG | CCTTCCCCTC | 120 |
| CGCCTCAATG | CAGAACCAANT | AGTGGGAGCA | CTGTGTTTAG | AGTTAAGAGT | GAACACTGTN | 180 |
| TGATTTTACT | TGGGAATTTT | CTCTGTTATA | TAGCTTTTCC | CAATGCTAAT | TTCCAAACAA | 240 |
| CAACAACAAA | ATAACATGTT | TGCCTGTINA | GTTGTATAAA | AGTANGTGAT | TCTGTATNTA | 300 |
| AAGAAAATAT | TACTGTTACA | TATACTGCTT | GCAANTTCTG | TATTTATTGG | TNCTCTGGAA | 360 |
| ATAAATATAT | TATTAAA | | | | | 377 |

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCCTTTGAGG | GGTTAGGGTC | CAGTTCACAG | TGGAAGAAAC | AGGCCAGGAG | AANTGCGTGC | 60 |
| CGAGCTGANG | CAGATTTCCC | ACAGTGACCC | CAGAGCCCTG | GGCTATAGTC | TCTGACCCCT | 120 |
| CCAAGGAAAG | ACCACCTTCT | GGGGACATGG | GCTGGAGGGC | AGGACCTAGA | GGCACCAGG | 180 |
| GAAGGCCCCA | TTCCGGGGCT | GTTCCCCGAG | GAGGAAGGGA | AGGGGCTCTG | TGTGCCCCCC | 240 |
| ACGAGGAANA | GGCCCTGANT | CCTGGGATCA | NACACCCCTT | CACGTGTATC | CCCACACAAA | 300 |
| TGCAAGCTCA | CCAAGGTCCC | CTCTCAGTCC | CTTCCCTACA | CCCTGAACGG | NCACTGGCCC | 360 |
| ACACCCACCC | AGANCANCCA | CCCGCCATGG | GGAATGTNCT | CAAGGAATCG | CNGGGCAACG | 420 |
| TGGACTCTNG | TCCCNNAAGG | GGGCAGAATC | TCCAATAGAN | GGANNGAACC | CTTGCTNANA | 480 |
| AAAAAAAANA | AAAAA | | | | | 495 |

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
GGTACTTGG TTTCAATTGCC ACCACTTAGT GGATGTCATT TAGAACCATT TTGTCTGCTC      60
CCTCTGGAAG CCTTGCAGCAG AGCGGACTTT GTAATTGTTG GAGAATAACT GCTGAATTTT      120
TAGCTGTTTT GAGTTGATTC GCACCACTGC ACCACAACCTC AATATGAAAA CTATTTNACT      180
TATTTATTAT CTTGTGAAAA GTATACAATG AAAATTTTGT TCATACTGTA TTTATCAAGT      240
ATGATGAAAA GCAATAGATA TATATTCTTT TATTATGTTN AATTATGATT GCCATTATTA      300
ATCGGCAAAA TGTGGAGTGT ATGTTCTTTT CACAGTAATA TATGCCTTTT GTAACCTCAC      360
TTGGTTATTT TATTGTAAAT GAATTACAAA ATTCTTAATT TAAGAAAATG GTANGTTATA      420
TTTANTTCAN TAATTTCTTT CCTTGTTTAC GTTAATTTTG AAAAGAATGC AT              472
```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```
CTGAAGCATT TCTTCAAACCT TNTCTACTTT TGTCATTGAT ACCTGTAGTA AGTTGACAAT      60
GTGGTGAAAT TTCAAAATTA TATGTAACCT CTACTAGTTT TACTTTCTCC CCCAAGTCTT      120
TTTTAACTCA TGATTTTTCAC ACACACAATC CAGAACTTAT TATATAGCCT CTAAGTCTTT      180
ATTCTTCACA GTAGATGATG AAAGAGTCCT CCAAGTGTCTT GNGCANAATG TTCTAGNTAT      240
AGCTGGATAC ATACNGTGGG AGTTCTATAA ACTCATACCT CAGTGGGACT NAACCAAAAT      300
TGTGTTAGTC TCAATTCCTA CCACACTGAG GGAGCCTCCC AAATCACTAT ATTCTTATCT      360
GCAGGTACTC CTCCAGAAAA ACNGACAGGG CAGGCTTGCA TGAAAAAGTN ACATCTGCGT      420
TACAAAGTCT ATCTTCCTCA NANGTCTGTN AAGGAACAAT TTAATCTTCT AGCTTT      476
```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```
ACTCTTTCTA ATGCTGATAT GATCTTGAGT ATAAGAATGC ATATGTCACCT AGAATGGATA      60
```

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AAATAATGCT | GCAAACCTAA | TGTTCTTATG | CAAAATGGAA | CGCTAATGAA | ACACAGCTTA | 120 |
| CAATCGCAAA | TCAAAACTCA | CAAGTGCTCA | TCTGTTGTAG | ATTTAGTGTA | ATAAGACTTA | 180 |
| GATTGTGCTC | CTTCGGATAT | GATTGTTTCT | CANATCTTGG | GCAATNTTCC | TTAGTCAAAT | 240 |
| CAGGCTACTA | GAATTCTGTT | ATTGGATATN | TGAGAGCATG | AAATTTTTAA | NAATACACTT | 300 |
| GTGATTATNA | AATTAATCAC | AAATTTCACT | TATACCTGCT | ATCAGCAGCT | AGAAAAACAT | 360 |
| NTNNTTTTAA | NATCAAAGTA | TTTTGTGTTT | GGAANTGTNN | AAATGAAATC | TGAATGTGGG | 420 |
| TTCNATCTTA | TTTTTCCCN | GACNACTANT | TNCTTTTTTA | GGGNCTATTC | TGANCCATC | 479 |

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGTGACTTGT | CCTCCAACAA | AACCCCTTGA | TCAAGTTTGT | GGCACTGACA | ATCAGACCTA | 60 |
| TGCTAGTTCC | TGTCATCTAT | TCGCTACTAA | ATGCAGACTG | GAGGGGACCA | AAAAGGGGCA | 120 |
| TCAACTCCAG | CTGGATTATT | TTGGAGCCTG | CAAATCTATT | CCTACTTGTA | CGGACTTTGA | 180 |
| AGTGATTCAG | TTTCCTCTAC | GGATGAGAGA | CTGGCTCAAG | AATATCCTCA | TGCAGCTTTA | 240 |
| TGAAGCCACT | CTGAACACGC | TGGTTATCTA | GATGAGAACA | GAGAAATAAA | GTCAGAAAAT | 300 |
| TTACCTGGAG | AAAAGAGGCT | TTGGCTGGGG | ACCATCCCAT | TGAACCTTCT | CTTAAGGACT | 360 |
| TTAAGAAAAA | CTACCACATG | TTGTGTATCC | TGGTGCCGGC | CGTTTATGAA | CTGACCACCC | 420 |
| TTTGGAATAA | TCTTGACGCT | CCTGAACCTG | CTCCTCTGCG | A | | 461 |

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTGGCCGCGC | GCAGGTGTTT | CCTCGTACCG | CAGGGCCCCC | TCCCTTCCCC | AGGCGTCCCT | 60 |
| CGGCGCCTCT | GCGGGCCCGA | GGAGGAGCGG | CTGGCGGGTG | GGGGGAGTGT | GACCCACCCT | 120 |
| CGGTGAGAAA | AGCCTTCTCT | AGCGATCTGA | GAGGCGTGCC | TTGGGGGTAC | C | 171 |

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGCGCAAG | TGCAACTCCA | GCTGGGGCCG | TGCGGACGAA | GATTCTGCCA | GCAGTTGGTC | 60 |
| CGACTGCGAC | GACGGCGGCG | GCGACAGTCG | CAGGTGCAGC | GCGGGCGCCT | GGGGTCTTGC | 120 |
| AAGGCTGAGC | TGACGCCGCA | GAGGTCGTGT | CACGTCCCAC | GACCTTGACG | CCGTCGGGGA | 180 |
| CAGCGCGAAC | AGAGCCCGGT | GAAGCGGGAG | GCCTCGGGGA | GCCCCTCGGG | AAGGGCGGCC | 240 |
| CGACAGATAC | GCAAGTGCAG | GTAGCCCGCC | | | | 269 |

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

| | | | | | | |
|------------|------------|------------|--------------|------------|--------------|-----|
| TTTTTTTTTT | TTTGGAAATC | TACTGCGAGC | ACAGCAGGTC | AGCAACAAGT | TTATTTTGCA | 60 |
| GCTAGCAAGG | TAACAGGGTA | GGGCATGGTT | ACATGTTTCTAG | GTCAACTTCC | TTTGTCTGGTGG | 120 |
| TTGATTGGTT | TGTCTTTATG | GGGGCGGGGT | GGGGTAGGGG | AAACGAAGCA | AATAACATGG | 180 |
| AGTGGGTGCA | CCCTCCCTGT | AGAACCTGGT | TACAAAGCTT | GGGGCAGTTC | ACCTGGTCTG | 240 |
| TGACCGTCAT | TTCTTGACA | TCAATGTTAT | TAGAAGTCAG | GATATCTTTT | AGAGAGTCCA | 300 |
| CTGTTCTGGA | GGGAGATTAG | GGTTTCTTGC | AAAATCCAAC | AAAATCCACT | GAAAAAGTTG | 360 |
| GATGATCAGT | ACGAATACCG | AGGCATATTC | TCATATCGGT | GGCCA | | 405 |

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | TTTTTTTTTT | 60 |
| GGCACTTAAT | CCATTTTTAT | TTCAAAATGT | CTACAAATTT | AATCCCATTA | TACGGTATTT | 120 |
| TCAAAATCTA | AATTATTCAA | ATTAGCCAAA | TCCTTACCAA | ATAATACCCA | AAAATCAAAA | 180 |
| ATATACTTCT | TTCAGCAAAC | TGTTTACATA | AATTAAAAAA | ATATATACGG | CTGGTGTTTT | 240 |
| CAAAGTACAA | TTATCTTAAC | ACTGCAAACA | TTTTAAGGAA | CTAAAAATAA | AAAAAACACT | 300 |
| CCGCAAAGGT | TAAAGGGAAC | AACAAATTCT | TATCAACAC | CATTATAAAA | ATCATATCTC | 360 |
| AAATCTTAGG | GGAAATATATA | CTTCACACGG | GGTCTTAAC | TTTACTCACT | TTGTTTATTT | 420 |
| TTTTAAACCA | TGTGTTGGGC | CCAACACAAT | GGAATCCCCC | CTGGACTAGT | | 470 |

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTGA | CCCCCTCTT | ATAAAAACA | AGTTACCATT | TTATTTTACT | 60 |
| TACACATATT | TATTTTATAA | TTGGTATTAG | ATATTCAAAA | GGCAGCTTTT | AAAATCAAAC | 120 |
| TAAATGGAAA | CTGCCTTAGA | TACATAATTC | TTAGGAATTA | GCTTAAAATC | TGCCTAAAGT | 180 |
| GAAAATCTTC | TCTAGCTCTT | TTGACTGTAA | ATTTTGGACT | CTTGTAACAA | ATCCAAATTC | 240 |
| ATTTTCTTGG | TCTTTAAAT | TATCTAATCT | TTCCATTTTT | TCCCTATTCC | AAGTCAATTT | 300 |
| GCTTCTCTAG | CCTCATTTCC | TAGCTCTTAT | CTACTATTAG | TAAGTGGCTT | TTTCCTAAA | 360 |
| AGGGAACA | GGAAGAGAAA | TGGCACACA | AACAAACATT | TTATATTCAT | ATTTCTACCT | 420 |
| ACGTTAATAA | AATAGCATT | TGTGAAGCCA | GCTCAAAAGA | AGGCTTAGAT | CCTTTTATGT | 480 |
| CCATTTTAGT | CACTAAACGA | TATCAAAGTG | CCAGAATGCA | AAAGGTTTGT | GAACATTTAT | 540 |
| TCAAAAGCTA | ATATAAGATA | TTTCACATAC | TCATCTTTCT | G | | 581 |

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTTTTT | TTTTTCTCTT | CTTTTTTTTT | GAAATGAGGA | TCGAGTTTTT | 60 |
| CACTCTCTAG | ATAGGGCATG | AAGAAAACCTC | ATCTTTCCAG | CTTTAAAATA | ACAATCAAAT | 120 |
| CTCTTATGCT | ATATCATATT | TTAAGTTAAA | CTAATGAGTC | ACTGGCTTAT | CTTCTCCTGA | 180 |
| AGGAAATCTG | TTCATTCTTC | TCATTCATAT | AGTTATATCA | AGTACTACCT | TGCATATTGA | 240 |
| GAGGTTTTTC | TTCTCTATTT | ACACATATAT | TTCCATGTGA | ATTTGTATCA | AACCTTTATT | 300 |
| TTTCATGCAA | CTAGAAAATA | ATGTTTCTTT | TGCATAAGAG | AAGAGAACAA | TATAGCATT | 360 |
| CAAACTGCT | CAAATTGTTT | GTTAAGTTAT | CCATTATAAT | TAGTTGGCAG | GAGCTAATAC | 420 |
| AAATCACATT | TACGACAGCA | ATAATAAAC | TGAAGTACCA | GTTAAATATC | CAAAATAATT | 480 |
| AAAGGAACAT | TTTAGCCTG | GGTATAATTA | GCTAATTCAC | TTTACAAGCA | TTTATTAGAA | 540 |
| TGAATTCACA | TGTTATTATT | CCTAGCCCAA | CACAATGG | | | 578 |

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTCAGTA | ATAATCAGAA | CAATATTTAT | TTTTATATTT | AAAATTCATA | 60 |
| GAAAAGTGCC | TTACATTTAA | TAAAAGTTTG | TTTCTCAAAG | TGATCAGAGG | AATTAGATAT | 120 |
| GTCTTGAACA | CCAATATTAA | TTTGAGGAAA | ATACACCAA | ATACATTAA | TAAATTATTT | 180 |
| AAGATCATAG | AGCTTGTAAG | TGAAAAGATA | AAATTTGACC | TCAGAAACTC | TGAGCATTAA | 240 |
| AAATCCACTA | TTAGCAAATA | AATTACTATG | GACTTCTTGC | TTTAATTTTG | TGATGAATAT | 300 |
| GGGGTGTAC | TGGTAAACCA | ACACATTCTG | AAGGATACAT | TACTTAGTGA | TAGATTCTTA | 360 |
| TGTACTTTGC | TAATACGTGG | ATATGAGTTG | ACAAGTTTCT | CTTTCTTCAA | TCTTTTAAGG | 420 |
| GGCGAGAAAT | GAGGAAGAAA | AGAAAAGGAT | TACGCATACT | GTTCTTTCTA | TGGAAGGATT | 480 |
| AGATATGTTT | CCTTTGCCAA | TATTAAAAAA | ATAATAATGT | TTACTACTAG | TGAAACCC | 538 |

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTTAGTC | AAGTTTCTAT | TTTTATTATA | ATTAAAGTCT | TGGTCATTTT | 60 |
| ATTTATTAGC | TCTGCAACTT | ACATATTTAA | ATTAAAGAAA | CGTTTTAGAC | AACTGTACAA | 120 |
| TTTATAAATG | TAAGGTGCCA | TTATTGAGTA | ATATATTCCT | CCAAGAGTGG | ATGTGTCCCT | 180 |
| TCTCCCACCA | ACTAATGAAC | AGCAACATTA | GTTTAATTTT | ATTAGTAGAT | ATACACTGCT | 240 |
| GCAAACGCTA | ATTCTCTTCT | CCATCCCCAT | GTGATATTGT | GTATATGTGT | GAGTTGGTAG | 300 |
| AATGCATCAC | AATCTACAAT | CAACAGCAAG | ATGAAGCTAG | GCTGGGCTTT | CGGTGAAAT | 360 |
| AGACTGTGTC | TGTCTGAATC | AAATGATCTG | ACCTATCCTC | GGTGGCAAGA | ACTCTTCGAA | 420 |
| CCGCTTCCTC | AAAGGCGCTG | CCACATTTGT | GGCTCTTTGC | ACTTGTTTCA | AAA | 473 |

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGCCATGGCA | CTGCAGGCA | TCTCGGTCAT | GGAGCTGTCC | GGCCTGGCCC | CGGGCCCGTT | 60 |
| CTGTGCTATG | GTCCTGGCTG | ACTTCGGGGC | GCGTGTGGTA | CGCGTGGACC | GGCCCGGCTC | 120 |
| CCGCTACGAC | GTGAGCCGCT | TGGGCCGGGG | CAAGCGCTCG | CTAGTGTGG | ACCTGAAGCA | 180 |
| GCCGCGGGGA | GCCGCCGTGC | TGCGGCGTCT | GTGCAAGCGG | TGGATGTGC | TGCTGGAGCC | 240 |
| CTTCCGCCGC | GGTGTATG | AGAACTCCA | GCTGGGCCCA | GAGATTCTGC | AGCGGGAAAA | 300 |
| TCCAAGGCTT | ATTTATGCCA | GGCTGAGTGG | ATTTGGCCAG | TCAGGAAGCT | TCTGCCGGTT | 360 |
| AGCTGGCCAC | GATATCAACT | ATTTGGCTTT | GTCAGGTGTT | CTCTCAAAAA | TTGGCAGAAG | 420 |
| TGGTGAGAAT | CCGTATGCCC | CGCTGAATCT | CCTGGCTGAC | TTTGCTGGTG | GTGGCCTTAT | 480 |
| GTGTGCACTG | GGCATTATAA | TGGCTCTTTT | TGACCGACA | CGCACTGACA | AGGGTCAGGT | 540 |

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CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTTCTGT GGAAAACTCA      600
GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTTT      660
CTATACGACT TACAGGACAG CAGATGGGGA ATTCATGGCT GTTGGAGCAA TAGAACCCCA      720
GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACTTC CCAATCAGAT      780
GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTTGCA GATGTATTTG CAAAGAAGAC      840
GAAGGCAGAG TGGTGTCAAA TCTTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC      900
TTTTGAGGAG GTTGTTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTTA TCACCAGTGA      960
GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTTA AACACCCCAG CCATCCCTTC     1020
TTTCAAAAGG GATCCTTTCA TAGGAGAACA CACTGAGGAG ATACTTGAAG AATTGGAATT     1080
CAGCCGCGAA GAGATTTATC AGCTTAATC AGATAAATC ATTGAAAGTA ATAAGGTAAA     1140
AGCTAGTCTC TAACTTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG     1200
TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTA CAGTGTCCCTA     1260
CCACTCTAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCTAAA     1320
AATGGTTATC ATTAGGGCTT TTGATTTATA AAACCTTGGG TACTTATACT AAATTATGGT     1380
AGTTATTCTG CCTTCCAGTT TGCTTGATAT ATTTGTTGAT ATTAAGATTG TTGACTTATA     1440
TTTCTGAATGG GTTCTAGTGA AAAAGGAATG ATATATTCCT GAAGACATCG ATATACATTT     1500
ATTTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGAT     1560
AAAAGTCACG TGAAACAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA     1620
A                                                                                   1621

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
1           5           10           15
Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
20           25           30
Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
35           40           45
Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
50           55           60
Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
65           70           75           80
Arg Arg Gly Val Met Glu Lys Leu Gln Leu Gly Pro Glu Ile Leu Gln
85           90           95
Arg Glu Asn Pro Arg Leu Ile Tyr Ala Arg Leu Ser Gly Phe Gly Gln
100          105          110
Ser Gly Ser Phe Cys Arg Leu Ala Gly His Asp Ile Asn Tyr Leu Ala
115          120          125
Leu Ser Gly Val Leu Ser Lys Ile Gly Arg Ser Gly Glu Asn Pro Tyr
130          135          140
Ala Pro Leu Asn Leu Leu Ala Asp Phe Ala Gly Gly Gly Leu Met Cys
145          150          155          160
Ala Leu Gly Ile Ile Met Ala Leu Phe Asp Arg Thr Arg Thr Asp Lys
165          170          175
Gly Gln Val Ile Asp Ala Asn Met Val Glu Gly Thr Ala Tyr Leu Ser
180          185          190
Ser Phe Leu Trp Lys Thr Gln Lys Ser Ser Leu Trp Glu Ala Pro Arg
195          200          205

```

Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
 210 215 220
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
 225 230 235 240
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
 245 250 255
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
 260 265 270
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
 275 280 285
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
 290 295 300
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
 305 310 315 320
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
 325 330 335
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
 340 345 350
 Ile Leu Glu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
 355 360 365
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|------|
| GGCAGGAGGC | TGCCCCAGGG | CCTGAGCGGA | GGCGGGGGCA | GCCTCGCCAG | CGGGGGCCCC | 60 |
| GGGCCTGGCC | ATGCCTCACT | GAGCCAGCGC | CTGCGCCTCT | ACCTCGCCGA | CAGCTGGAAC | 120 |
| CAGTGCAGAC | TAGTGGCTCT | CACCTGCTTC | CTCCTGGGCG | TGGGCTGCCG | GCTGACCCCG | 180 |
| GGTTTGATAC | ACCTGGGCGG | CACCTGCTTC | TGCATCGACT | TCATGGTTTT | CACGGTGCCG | 240 |
| CTGCTTCACA | TCTTCACGGT | CAACAAACAG | CTGGGGCCCC | AGATCGTCAT | CGTGAGCAAG | 300 |
| ATGATGAAGG | ACGTGTTCTT | CTTCTCTTTC | TTCTTCGGCG | TGTGGCTGGT | AGCCTATGGC | 360 |
| GTGGCCACGG | AGGGGCTCCT | GAGGCCACGG | GACAGTGACT | TCCCAAGTAT | CCTGCGCCGC | 420 |
| GTCTTCTACC | GTCCCTACCT | GCAGATCTTC | GGGCAGATTC | CCCAGGAGGA | CATGGACGTG | 480 |
| GCCCTCATGG | AGCACAGCAA | CTGCTCGTCG | GAGCCC GGCT | TCTGGGCACA | CCCTCCTGGG | 540 |
| GCCCAGGCGG | GCACCTGCGT | CTCCCACTAT | GCCAACCTGGC | TGGTGGTGCT | GCTCCTCGTC | 600 |
| ATCTTCTGCT | TCGTGGCCAA | CATCCTGCTG | GTCAACTTGC | TCATTGCCAT | GTTCACTTAC | 660 |
| ACATTCGGCA | AAGTACAGGG | CAACAGCGAT | CTCTACTGGA | AGGCGCAGCG | TTACCGCCTC | 720 |
| ATCCGGGAAT | TCCACTCTCG | GCCCCGCGCT | GCCCCGCCCT | TTATCGTCAT | CTCCCACTTG | 780 |
| CGCCTCCTGC | TCAGGCAATT | GTGCAGGCGA | CCCCGGAGCC | CCCAGCCGTC | CTCCCGGCC | 840 |
| CTCGAGCATT | TCCGGGTTTA | CCTTTCTAAG | GAAGCCGAGC | GGAAGCTGCT | AACGTGGGAA | 900 |
| TCGGTGATA | AGGAGAACTT | TCTGCTGGCA | CGCGCTAGGG | ACAAGCGGGA | GAGCGACTCC | 960 |
| GAGCGTCTGA | AGCGCACGTC | CCAGAAGGTG | GACTTGGCAC | TGAAACAGCT | GGGACACATC | 1020 |
| CGCGAGTACG | AACAGCGCCT | GAAAGTGCTG | GAGCGGGAGG | TCCAGCAGTG | TAGCCGCGTC | 1080 |
| CTGGGGTGCG | TGGCCGAGGC | CCTGAGCCGC | TCTGCCTTGC | TGCCCCCAGG | TGGGCCGCCA | 1140 |
| CCCCCTGACC | TGCCTGGGTC | CAAAGACTGA | GCCCTGCTGG | CGGACTTCAA | GGAGAAGCCC | 1200 |
| CCACAGGGGA | TTTTGCTCCT | AGAGTAAGGC | TCATCTGGGC | CTCGGCCCCC | GCACCTGGTG | 1260 |
| GCCTTGTCCT | TGAGGTGAGC | CCCATGTCCA | TCTGGGCCAC | TGTCAGGACC | ACCTTTGGGA | 1320 |
| GTGTCATCCT | TACAAACCAC | AGCATGCCCC | GCTCCTCCCA | GAACCAGTCC | CAGCCTGGGA | 1380 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GGATCAAGGC | CTGGATCCCG | GGCCGTTATC | CATCTGGAGG | CTGCAGGGTC | CTTGGGGTAA | 1440 |
| CAGGGACCAC | AGACCCCTCA | CCACTCACAG | ATTCTCACA | CTGGGAAAT | AAAGCCATTT | 1500 |
| CAGAGGAAAA | AAAAAAAAAA | AAAA | | | | 1524 |

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| GGGAACCAGC | CTGCACGCGC | TGGCTCCGGG | TGACAGCCGC | GCGCCTCGGC | CAGGATCTGA | 60 |
| GTGATGAGAC | GTGTCCCCAC | TGAGGTGCC | CACAGCAGCA | GGTGTGAGC | ATGGGCTGAG | 120 |
| AAGCTGGACC | GGCACCAAAG | GGCTGGCAGA | AATGGGCGCC | TGGCTGATTC | CTAGGCAGTT | 180 |
| GGCGGCAGCA | AGGAGGAGAG | GCCGCAGCTT | CTGGAGCAGA | GCCGAGACGA | AGCAGTTCTG | 240 |
| GAGTGCCTGA | ACGGCCCCCT | GAGCCCTACC | CGCCTGGCCC | ACTATGGTCC | AGAGGCTGTG | 300 |
| GGTGAGCCGC | CTGCTGCGGC | ACCGGAAAGC | CCAGCTCTTG | CTGGTCAACC | TGCTAACCTT | 360 |
| TGGCCTGGAG | GTGTGTTTGG | CCGCAGGCAT | CACCTATGTG | CCGCCTCTGC | TGCTGGAAGT | 420 |
| GGGGGTAGAG | GAGAAGTTCA | TGACCATGGT | GCTGGGCATT | GGTCCAGTGC | TGGGCCTGGT | 480 |
| CTGTGTCCCG | CTCCTAGGCT | CAGCCAGTGA | CCACTGGCGT | GGACGCTATG | GCCGCCGCCG | 540 |
| GCCCTTCATC | TGGGCACGTG | CCTTGGGCAT | CCTGCTGAGC | CTCTTTCTCA | TCCAAGGGC | 600 |
| CGGCTGGCTA | GCAGGGCTGC | TGTGCCCGGA | TCCCAGGCC | CTGGAGCTGG | CACTGCTCAT | 660 |
| CCTGGGCGTG | GGGCTGCTGG | ACTTCTGTGG | CCAGGTGTGC | TCACTCCAC | TGGAGGCCCT | 720 |
| GCTCTCTGAC | CTCTTCCGGG | ACCCGGACCA | CTGTCGCCAG | GCCTACTCTG | TCTATGCCCT | 780 |
| CATGATCAGT | CTTGGGGGCT | GCCTGGGCTA | CCTCCTGCCT | GCCATTGACT | GGGACACCAG | 840 |
| TGCCCTGGCC | CCCTACCTGG | GCACCCAGGA | GGAGTGCCTC | TTTGGCCTGC | TCACCCTCAT | 900 |
| CTTCTCACC | TGCGTAGCAG | CCACACTGCT | GGTGGCTGAG | GAGGCAGCGC | TGGGCCCCAC | 960 |
| CGAGCCAGCA | GAAGGGCTGT | CGGCCCCCTC | CTGTGCGCCC | CACTGCTGTC | CATGCCGGGC | 1020 |
| CCGCTTGGCT | TTCCGGAACC | TGGGCGCCCT | GCTTCCCCGG | CTGCACCAGC | TGTGCTGCCG | 1080 |
| CATGCCCCGC | ACCCTGCGCC | GGCTCTTCGT | GGCTGAGCTG | TGCAGCTGGA | TGGCACTCAT | 1140 |
| GACCTTCACG | CTGTTTTACA | CGGATTTTCG | GGGCGAGGGG | CTGTACCAGG | GCGTGCCCAG | 1200 |
| AGCTGAGCCG | GGCACCGAGG | CCCGGAGACA | CTATGATGAA | GGCGTTCGGA | TGGGCAGCCT | 1260 |
| GGGGCTGTTC | CTGCAGTGCG | CCATCTCCCT | GGTCTTCTCT | CTGGTCATGG | ACCGGCTGGT | 1320 |
| GCAGCGATTG | CGCACTCAGG | CAGTCTATTT | GGCCAGTGTG | GCAGCTTTCC | CTGTGGCTGC | 1380 |
| CGGTGCCACA | TGCCTGTCCC | ACAGTGTGGC | CGTGGTGACA | GCTTCAGCCG | CCCTCACCAG | 1440 |
| GTTACACCTT | TCAGCCCTGC | AGATCCTGCC | CTACACACTG | GCCTCCCTCT | ACCACCGGGA | 1500 |
| GAAGCAGGTG | TTCTTGCCCA | AATACCGAGG | GGACACTGGA | GGTGCTAGCA | GTGAGGACAG | 1560 |
| CCTGATGACC | AGCTTCCTGC | CAGGCCCTAA | GCCTGGAGCT | CCCTTCCCTA | ATGGACACGT | 1620 |
| GGGTGCTGGA | GGCAGTGGCC | TGCTCCCACC | TCCACCCGCG | CTCTGCGGGG | CCTCTGCCTG | 1680 |
| TGATGTCTCC | GTACGTGTGG | TGGTGGGTGA | GCCCACCGAG | GCCAGGGTGG | TTCCGGGGCCG | 1740 |
| GGGCATCTGC | CTGGACCTCG | CCATCCTGGA | TAGTGCCTTC | CTGCTGTCCC | AGGTGGCCCC | 1800 |
| ATCCCTGTTT | ATGGGCTCCA | TTGTCCAGCT | CAGCCAGTCT | GTCACTGCCT | ATATGGTGTG | 1860 |
| TGCCGCAGGC | CTGGGTCTGG | TCGCCATTTA | CTTTGCTACA | CAGGTAGTAT | TTGACAAGAG | 1920 |
| CGACTTGGCC | AAATACTCAG | CGTAGAAAAC | TTCCAGCACA | TTGGGGTGGA | GGGCCTGCCT | 1980 |
| CACTGGGTCC | CAGCTCCCCG | CTCCTGTTAG | CCCCATGGGG | CTGCCGGGCT | GGCCGCCAGT | 2040 |
| TTCTGTTGCT | GCCAAAGTAA | TGTGGCTCTC | TGCTGCCACC | CTGTGCTGCT | GAGGTGCGTA | 2100 |
| GCTGCACAGC | TGGGGGCTGG | GGCGTCCCTC | TCCTCTCTCC | CCAGTCTCTA | GGGCTGCCTG | 2160 |
| ACTGGAGGCC | TTCCAAGGGG | GTTTCACTCT | GGACTTATAC | AGGGAGGCCA | GAAGGGCTCC | 2220 |
| ATGCACTGGA | ATGCGGGGAC | TCTGCAGGTG | GATTACCCAG | GCTCAGGGTT | AACAGCTAGC | 2280 |
| CTCCTAGTTG | AGACACACCT | AGAGAAGGGT | TTTTGGGAGC | TGAATAAACT | CAGTCACCTG | 2340 |
| GTTTCCCATC | TCTAAGCCCC | TTAACCTGCA | GCTTCGTTTA | ATGTAGCTCT | TGCATGGGAG | 2400 |
| TTTCTAGGAT | GAAACACTCC | TCCATGGGAT | TTGAACATAT | GACTTATTTG | TAGGGGAAGA | 2460 |
| GTCCTGAGGG | GCAACACACA | AGAACCAGGT | CCCCCTAGCC | CACAGCACTG | TCTTTTGTCT | 2520 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GATCCACCCC | CCTCTTACCT | TTTATCAGGA | TGTGGCCTGT | TGGTCCTTCT | GTTGCCATCA | 2580 |
| CAGAGACACA | GGCATTTAAA | TATTTAACTT | ATTATTTTAA | CAAAGTAGAA | GGGAATCCAT | 2640 |
| TGCTAGCTTT | TCTGTGTTGG | TGTCTAATAT | TTGGGTAGGG | TGGGGGATCC | CCAACAATCA | 2700 |
| GGTCCCCTGA | GATAGCTGGT | CATTGGGCTG | ATCATTGCCA | GAATCTTCTT | CTCCTGGGGT | 2760 |
| CTGGCCCCC | AAAATGCCTA | ACCCAGGACC | TTGGAAATTC | TACTCATCCC | AAATGATAAT | 2820 |
| TCCAAATGCT | GTTACCCAAG | GTTAGGGTGT | TGAAGGAAGG | TAGAGGGTGG | GGCTTCAGGT | 2880 |
| CTCAACGGCT | TCCCTAACCA | CCCCCTTCT | CTTGGCCCAG | CCTGGTTCCC | CCCACCTCCA | 2940 |
| CTCCCCTCTA | CTCTCTCTAG | GACTGGGCTG | ATGAAGGCAC | TGCCCAAAAT | TTCCCCTACC | 3000 |
| CCCAACTTTC | CCCTACCCCC | AACTTTCCCC | ACCAGCTCCA | CAACCCTGTT | TGGAGCTACT | 3060 |
| GCAGGACCAG | AAGCACAAAG | TGCGGTTTCC | CAAGCCTTTG | TCCATCTCAG | CCCCCAGAGT | 3120 |
| ATATCTGTGC | TTGGGGAATC | TCACACAGAA | ACTCAGGAGC | ACCCCTGCC | TGAGCTAAGG | 3180 |
| GAGGTCTTAT | CTCTCAGGGG | GGGTTTAAGT | GCCGTTTGCA | ATAATGTCGT | CTTATTTATT | 3240 |
| TAGCGGGGTG | AATATTTTAT | ACTGTAAGTG | AGCAATCAGA | GTATAATGTT | TATGGTGACA | 3300 |
| AAATTAAAGG | CTTTCTTATA | TGTTTAAAAA | AAAAAAAAAA | AAAAAAAAAA | AAAAAAAAAA | 3360 |
| AAAAAAAAAA | AAAAAAAAAA | AAAAAAAAAA | AAAAAATAA | AAAAAAAAAA | | 3410 |

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|------|
| AGCCAGGCGT | CCCTCTGCCT | GCCCACTCAG | TGGCAACACC | CGGGAGCTGT | TTTGTCTTTT | 60 |
| GTGGAGCCTC | AGCAGTTCCC | TCTTTCAGAA | CTCACTGCCA | AGAGCCCTGA | ACAGGAGCCA | 120 |
| CCATGCAGTG | CTTCAGCTTC | ATTAAAGACCA | TGATGATCCT | CTTCAATTTG | CTCATCTTTT | 180 |
| TGTGTGGTGC | AGCCCTGTTG | GCAGTGGGCA | TCTGGGTGTC | AATCGATGGG | GCATCCTTTC | 240 |
| TGAAGATCTT | CGGGCCACTG | TCGTCCAGTG | CCATGCAGTT | TGTCAACGTG | GGCTACTTCC | 300 |
| TCATCGCAGC | CGGCGTTGTG | GTCTTTGCTC | TTGGTTTCCT | GGGCTGCTAT | GGTGCTAAGA | 360 |
| CTGAGAGCAA | GTGTGCCCTC | GTGACGTTCT | TCTTCATCCT | CCTCCTCATC | TTCATTGCTG | 420 |
| AGGTTGCAGC | TGCTGTGGTC | GCCTTGGTGT | ACACCACAAT | GGCTGAGCAC | TTCCCTGACGT | 480 |
| TGCTGGTAGT | GCCTGCCATC | AAGAAAGATT | ATGGTTCCCA | GGAAGACTTC | ACTCAAGTGT | 540 |
| GGAACACCAC | CATGAAAGGG | CTCAAGTGCT | GTGGCTTCAC | CAACTATACG | GATTTTGAGG | 600 |
| ACTCACCTTA | CTTCAAAGAG | AACAGTGCTT | TTCCCCCATT | CTGTTGCAAT | GACAACGTCA | 660 |
| CCAACACAGC | CAATGAAACC | TGCACCAAGC | AAAAGGCTCA | CGACCAAAAA | GTAGAGGGTT | 720 |
| GCTTCAATCA | GCTTTTGTAT | GACATCCGAA | CTAATGCAGT | CACCGTGGGT | GGTGTGGCAG | 780 |
| CTGGAATTGG | GGGCCTCGAG | CTGGCTGCCA | TGATTGTGTC | CATGTATCTG | TACTGCAATC | 840 |
| TACAATAAGT | CCACTTCTGC | CTCTGCCACT | ACTGCTGCCA | CATGGGAACT | GTGAAGAGGC | 900 |
| ACCCTGGCAA | GCAGCAGTGA | TTGGGGGAGG | GGACAGGATC | TAACAATGTC | ACTTGGGCCA | 960 |
| GAATGGACCT | GCCCTTTCTG | CTCCAGACTT | GGGGCTAGAT | AGGGACCACT | CCTTTTAGCG | 1020 |
| ATGCCTGACT | TTCTTTCCAT | TGGTGGGTGG | ATGGGTGGGG | GGCATTCCAG | AGCCTCTAAG | 1080 |
| GTAGCCAGTT | CTGTTGCCCA | TTCCCCCAGT | CTATTAAACC | CTTGATATGC | CCCCTAGGCC | 1140 |
| TAGTGGTGAT | CCAGTGCTC | TACTGGGGGA | TGAGAGAAAG | GCATTTTATA | GCCTGGGCAT | 1200 |
| AAGTGAAATC | AGCAGAGCCT | CTGGGTGGAT | GTGTAGAAGG | CACTTCAAAA | TGCATAAACC | 1260 |
| TGTTACAATG | TTAAAAAAA | AAAAAAA | | | | 1289 |

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1           5           10           15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
          20           25           30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
          35           40           45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
          50           55           60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
          65           70           75           80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
          85           90           95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
          100          105          110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Leu Val Ile Phe
          115          120          125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
          130          135          140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
          145          150          155          160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
          165          170          175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Leu Arg Gln
          180          185          190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
          195          200          205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
          210          215          220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
          225          230          235          240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
          245          250          255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
          260          265          270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
          275          280          285

```

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
 290 295 300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 553 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 1 5 10 15
 Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 20 25 30
 Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val
 35 40 45
 Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
 50 55 60
 Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
 65 70 75 80
 Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
 85 90 95
 Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
 100 105 110
 Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
 115 120 125
 Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140
 Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160
 Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175
 Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190
 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220
 Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240
 Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp

530

535

540

Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
 1 5 10 15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 20 25 30

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 35 40 45

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
 50 55 60

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
 65 70 75 80

Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
 85 90 95

Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
 100 105 110

Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
 115 120 125

Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
 130 135 140

Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
 145 150 155 160

Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
 165 170 175

Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
 180 185 190

His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
 195 200 205

Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
 210 215 220

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
 225 230 235 240

Gln

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCTCTTTCTC | TCCCCTCCTC | TGAATTTAAT | TCTTTCAACT | TGCAATTTGC | AAGGATTACA | 60 |
| CATTTCACTG | TGATGTATAT | TGTGTTGCAA | AAAAAAAAAA | GTGTCTTTGT | TTAAAATTAC | 120 |
| TTGGTTTGTG | AATCCATCTT | GCTTTTTCCT | CATTGGAAC | AGTCATTAC | CCATCTCTGA | 180 |
| ACTGGTAGAA | AAACATCTGA | AGAGCTAGTC | TATCAGCATC | TGACAGGTGA | ATTGGATGGT | 240 |
| TCTCAGAACC | ATTTACCCCA | GACAGCCTGT | TTCTATCCTG | TTTAATAAAT | TAGTTTGGGT | 300 |
| TCTCTACATG | CATAACAAAC | CCTGCTCCAA | TCTGTCACAT | AAAAGTCTGT | GACTTGAAGT | 360 |
| TTAGTC | | | | | | 366 |

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACAAAGATGA | ACCATTTCCT | ATATTATAGC | AAAATTAAAA | TCTACCCGTA | TTCTAATATT | 60 |
| GAGAAATGAG | ATNAAACACA | ATNTTATAAA | GTCTACTTAG | AGAAGATCAA | GTGACCTCAA | 120 |
| AGACTTTACT | ATTTTCATAT | TTTAAGACAC | ATGATTTATC | CTATTTTAGT | AACCTGGTTC | 180 |
| ATACGTTAAA | CAAAGGATAA | TGTGAACAGC | AGAGAGGATT | TGTTGGCAGA | AAATCTATGT | 240 |
| TCAATCTNGA | ACTATCTANA | TCACAGACAT | TTCTATTCTT | TT | | 282 |

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACACATGTCG | CTTCACTGCC | TTCTTAGATG | CTTCTGGTCA | ACATANAGGA | ACAGGGACCA | 60 |
| TATTTATCCT | CCCTCCTGAA | ACAATTGCAA | AATAANACAA | AATATATGAA | ACAATTGCAA | 120 |
| AATAAGGCAA | AATATATGAA | ACAACAGGTC | TCGAGATATT | GGAAATCAGT | CAATGAAGGA | 180 |
| TACTGATCCC | TGATCACTGT | CCTAATGCAG | GATGTGGGAA | ACAGATGAGG | TCACCTCTGT | 240 |
| GACTGCCCCA | GCTTACTGCC | TGTAGAGAGT | TTCTANGCTG | CAGTTCAGAC | AGGGAGAAAT | 300 |
| TGGGT | | | | | | 305 |

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

| | | | | | | |
|------------|------------|------------|------------|------------|----------|----|
| ACCAAGGTGT | NTGAATCTCT | GACGTGGGGA | TCTCTGATTC | CCGCACAATC | TGAGTGGA | 60 |
| AANTCCTGGG | T | | | | | 71 |

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTCCGGTTG | GTGTCAGCAG | CACGTGGCAT | TGAACATNGC | AATGTGGAGC | CCAAACCACA | 60 |
| GAAAATGGGG | TGAAATTGGC | CAACTTTCTA | TNAACTTATG | TTGGCAANTT | TGCCACCAAC | 120 |
| AGTAAGCTGG | CCCTTCTAAT | AAAAGAAAAT | TGAAAGGTTT | CTCACTAANC | GGAATTAANT | 180 |
| AATGGANTCA | AGANACTCCC | AGGCCTCAGC | GT | | | 212 |

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

```
ACTCGTTGCA NATCAGGGGC CCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC 60
CTCCGCCGGC GCAGAACATG CTGGGGTGGT 90
```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
TGTANCGTGA ANACGACAGA NAGGGTTGTC AAAAATGGAG AANCCTTGAA GTCATTTTGA 60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG 120
ATATNCANGT AAATTANGGA ATGAATTCAT GGTTCCTTTG GGAATTCCTT TACGATNGCC 180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA 218
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG 60
CATTTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT 120
CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCGG T 171
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA 60
TTATCAANTA TTGTGT 76

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT 60
CAATGTGCTG GGTCAATATG AGGGGAGGAG ACTCTAAAT AGCCAATTTT ATTCTCTTGG 120
TTAAGATTG T 131

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG 60
CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA 120
CTACAGTCTG CATTTGCGAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT 180
TTGCCTCACC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG 240
CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC 300
CATGGTGGGG GTCTTGCACT TGTAAGAATG GAATTGATTT TGCTTTTGCA AGAATCTCAG 360
CAGGAAACAT CAGAACCCT ATTTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC 420
CTCTTTGCTT GT 432

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

| | |
|---|-----|
| ACACAACCTTG AATAGTAAAA TAGAAACTGA GCTGAAATTT CTAATTCAC | 60 |
| AGTAAGAATG ATATTTCCCC CCAGGGATCA CCAAATATTT ATAAAAATTT GT | 112 |

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

| | |
|---|----|
| ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG | 54 |
|---|----|

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

| | |
|---|-----|
| ACCTCATTAG TAATTGTTTT GTTGTTTCAT TTTTTTCTAA TGTCTCCCCT CTACCAGCTC | 60 |
| ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTTGC TCTCTGCTCA | 120 |
| TTCTCTCTGA AGTCTAGGTT ACCCATTTTG GGGACCCATT ATAGGCAATA AACACAGTTC | 180 |
| CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTTT TCTTAGCCTT | 240 |
| TTCTTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT | 300 |
| AGGCTGCCTT CTTTTCCATG TCC | 323 |

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

| | |
|---|-----|
| ACATACATGT GTGTATATTT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATAC | 60 |
| TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCATC | 120 |

TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTTCAT TTCCTTCACG TTGGCCAATG 180
GATAAACAAA GT 192

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

| | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|-----|
| CCCTTTT | TTA | TGGAATGAGT | AGACTGTATG | TTTGAANATT | TANCCACAAC | CTCTTTGACA | 60 |
| TATAATGACG | CAACAAAAAG | GTGCTGTTA | GTCTATGGT | TCAGTTTATG | CCCCTGACAA | | 120 |
| GTTTCCATTG | TGTTTTGCCG | ATCTTCTGGC | TAATCGTGGT | ATCCTCCATG | TTATTAGTAA | | 180 |
| TTCTGTATTC | CATTTTGTTA | ACGCCTGGTA | GATGTAACT | GCTANGAGGC | TAACTTTATA | | 240 |
| CTTATTTAAA | AGCTCTTATT | TTGTGGTCAT | TAAAATGGCA | ATTTATGTGC | AGCACTTTAT | | 300 |
| TGCAGCAGGA | AGCACGTGTG | GTTTGGTTGT | AAAGCTCTT | GCTAATCTTA | AAAAGTAATG | | 360 |
| GG | | | | | | | 362 |

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTTTTTGAAA | GATCGTGTCC | ACTCCTGTGG | ACATCTTGTT | TTAATGGAGT | TTCCCATGCA | 60 |
| GTANGACTGG | TATGGTTGCA | GCTGTCCAGA | TAAAAACATT | TGAAGAGCTC | CAAAATGAGA | 120 |
| GTTCTCCCAG | GTTCGCCCTG | CTGCTCCAAG | TCTCAGCAGC | AGCCTCTTTT | AGGAGGCATC | 180 |
| TTCTGAACTA | GATTAAGGCA | GCTTGTAAT | CTGATGTGAT | TTGGTTTATT | ATCCAATAA | 240 |
| CTTCCATCTG | TTATCACTGG | AGAAAGCCCA | GACTCCCCAN | GACNGGTACG | GATTGTGGGC | 300 |
| ATANAAGGAT | TGGGTGAAGC | TGGCGTTGTG | GT | | | 332 |

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

| | |
|---|-----|
| ACTTTTGCCA TTTTGTATAT ATAAACAATC TTGGGACATT CTCCTGAAAA CTAGGTGTCC | 60 |
| AGTGGCTAAG AGAACTCGAT TTCAAGCAAT TCTGAAAGGA AAACCAGCAT GACACAGAAT | 120 |
| CTCAAATTCC CAAACAGGGG CTCTGTGGGA AAAATGAGGG AGGACCTTTG TATCTCGGGT | 180 |
| TTTAGCAAGT TAAATGAAN ATGACAGGAA AGGCTTATTT ATCAACAAAG AGAAGAGTTG | 240 |
| GGATGCTTCT AAAAAAACT TTGGTAGAGA AAATAGGAAT GCTNAATCCT AGGGAAGCCT | 300 |
| GTAACAATCT ACAATTGGTC CA | 322 |

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

| | |
|---|-----|
| ACAAGCCTTC ACAAGTTTAA CTAAATTGGG ATTAATCTTT CTGTANTTAT CTGCATAATT | 60 |
| CTTGTTTTTC TTTCCATCTG GTCCTGGGT TGACAATTTG TGGAAACAAC TCTATTGCTA | 120 |
| CTATTTAAAA AAAATCACAA ATCTTCCCT TTAAGCTATG TTNAATTCAA ACTATTCCTG | 180 |
| CTATTCCTGT TTTGTCAAAG AAATTATATT TTTCAAAATA TGTNTATTTG TTTGATGGGT | 240 |
| CCCACGAAAC ACTAATAAAA ACCACAGAGA CCAGCCTG | 278 |

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

| | |
|--|-----|
| GTTTANAAAA CTTGTTTAGC TCCATAGAGG AAAGAATGTT AAACTTTGTA TTTTAAACA | 60 |
| TGATTCTCTG AGGTAAACT TGGTTTTCAT ATGTTATTTT TACTTGATT TTGCTTTTGG | 120 |
| T | 121 |

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTTANAACC | ATGCCTAGCA | CATCAGAATC | CCTCAAAGAA | CATCAGTATA | ATCCTATACC | 60 |
| ATANCAAGTG | GTGACTGGTT | AAGCGTGCGA | CAAAGGTCAG | CTGGCACATT | ACTTGTGTGC | 120 |
| AAACTTGATA | CTTTTGTTC | AAGTAGGAAC | TAGTATACAG | TNCCTAGGAN | TGGTACTCCA | 180 |
| GGGTGCCCCC | CAACTCCTGC | AGCCGCTCCT | CTGTGCCAGN | CCCTGNAAGG | AACTTTCGCT | 240 |
| CCACCTCAAT | CAAGCCCTGG | GCCATGCTAC | CTGCAATTGG | CTGAACAAAC | GTTTGCTGAG | 300 |
| TTCCCAAGGA | TGCAAAGCCT | GGTGCTCAAC | TCCTGGGGCG | TCAACTCAGT | | 350 |

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TGTACCGTGA | AGACGACAGA | AGTTGCATGG | CAGGGACAGG | GCAGGGCCGA | GGCCAGGGTT | 60 |
| GCTGTGATTG | TATCCGAATA | NTCCTCGTGA | GAAAAGATAA | TGAGATGACG | TGAGCAGCCT | 120 |
| GCAGACTTGT | GTCTGCCTTC | AANAAGCCAG | ACAGGAAGGC | CCTGCCTGCC | TTGGCTCTGA | 180 |
| CCTGGCGGCC | AGCCAGCCAG | CCACAGGTGG | GCTTCTTCCT | TTTGTGGTGA | CAACNCCAAG | 240 |
| AAACTGTCAG | AGGCCCAGGG | TCAGGTGTNA | GTGGGTANGT | GACCATAAAA | CACCAGGTGC | 300 |
| TCCAGGAAC | CCGGGCAAAG | GCCATCCCCA | CCTACAGCCA | GCATGCCCAC | TGGCGTGATG | 360 |
| GGTGACAGANG | GATGAAGCAG | CCAGNTGTTC | TGCTGTGGT | | | 399 |

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTGGTGTGG | TNGGGGGTGA | TGCTGGTGGT | ANAAGTTGAN | GTGACTTCAN | GATGGTGTGT | 60 |
| GGAGGAAGTG | TGTGAACGTA | GGGATGTAGA | NGTTTGGCC | GTGCTAAATG | AGCTTCGGGA | 120 |
| TTGGCTGGTC | CCACTGGTGG | TCACTGTCAT | TGGTGGGGTT | CCTGT | | 165 |

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTCACTGGA | ATGCCACATT | CACAACAGAA | TCAGAGGTCT | GTGAAAACAT | TAATGGCTCC | 60 |
| TTAACTTCTC | CAGTAAGAAT | CAGGGACTTG | AAATGGAAAC | GTTAACAGCC | ACATGCCCAA | 120 |
| TGCTGGGCAG | TCTCCCATGC | CTTCCACAGT | GAAAGGGCTT | GAGAAAAATC | ACATCCAATG | 180 |
| TCATGTGTTT | CCAGCCACAC | CAAAAGGTGC | TTGGGGTGGA | GGGCTGGGGG | CATANANGGT | 240 |
| CANGCCTCAG | GAAGCCTCAA | GTTCCATTCA | GCTTTGCCAC | TGTACATTCC | CCATNTTTAA | 300 |
| AAAAACTGAT | GCCTTTTTTT | TTTTTTTTTG | TAAAATTG | | | 338 |

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GGGAATCTTG | GTTTTTGGCA | TCTGGTTTGC | CTATAGCCGA | GGCCACTTTG | ACAGAACAAA | 60 |
| GAAAGGGACT | TCGAGTAAGA | AGGTGATTTA | CAGCCAGCCT | AGTGCCCGAA | GTGAAGGAGA | 120 |
| ATTCAAACAG | ACCTCGTCAT | TCCTGGTGTG | AGCCTGGTCG | GCTCACC GCC | TATCATCTGC | 180 |
| ATTTGCCTTA | CTCAGGTGCT | ACCGGACTCT | GGCCCTGAT | GTCTGTAGTT | TCACAGGATG | 240 |
| CCTTATTTGT | CTTCTACACC | CCACAGGGCC | CCCTACTTCT | TCGGATGTGT | TTTTAATAAT | 300 |
| GTCAGCTATG | TGCCCCATCC | TCCTTCATGC | CCTCCCTCCC | TTTCCTACCA | CTGCTGAGTG | 360 |
| GCCTGGAAGT | TGTTTAAAGT | GT | | | | 382 |

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACCAANCTT | CTTTCTGTTG | TGTTNGATTT | TACTATAGGG | GTTTNGCTTN | TTCTAAANAT | 60 |
| ACTTTTCATT | TAACANCTTT | TGTTAAGTGT | CAGGCTGCAC | TTTGCTCCAT | ANAATTATTG | 120 |
| TTTTCACATT | TCAACTTGTA | TGTGTTTGTC | TCTTANAGCA | TTGGTGAAAT | CACATATTTT | 180 |
| ATATTCAGCA | TAAAGGAGAA | | | | | 200 |

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

| | |
|---|-----|
| ACTTTATTTT CAAACACTC ATATGTTGCA AAAACACAT AGAAAAATAA AGTTTGGTGG | 60 |
| GGGTGCTGAC TAAACTTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGTT | 120 |
| ATGCATGTAG AGAACCCAAA CTAATTTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA | 180 |
| AATGGTTCTG AGAACCATCC AATTCACCTG TCAGATGCTG ATANACTAGC TCTTCAGATG | 240 |
| TTTTTCTACC AGTTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATGG | 300 |
| ATTCACAAAC CAAGTAATTT TAAACAAAGA CACTT | 335 |

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

| | |
|---|-----|
| ACCAGGTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAAACAGA CGTGTATTTA | 60 |
| GGGTTGTTTA AAGACAACCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT | 120 |
| CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTTTA TTCAGATAGC AGTCTGATCA | 180 |
| CACATGGTCC AACAACACTC AAATAATAAA TCAAATATNA TCAGATGTTA AAGATTGGTC | 240 |
| TTCAAACATC ATAGCCAATG ATGCCCCGCT TGCCTATAAT CTCTCCGACA TAAAACCACA | 300 |
| TCAACACCTC AGTGGCCACC AAACCATCA GCACAGCTTC CTTAACTGTG AGCTGTTTGA | 360 |
| AGTACCAAGT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT | 420 |
| CAGCANGGGT GGGAGGAACC AGCTCAACCT TGGCGTANT | 459 |

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

| | |
|---|-----|
| ACATTTCTT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG | 60 |
| AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTCACCA ACCCCACCCA TCTCCCTGAG | 120 |
| ACCATCCGAC TTCCCTGTGT | 140 |

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

| | |
|---|-----|
| ACTTCAGTAA CAACATACAA TAACAACATT AAGTGTATAT TGCCATCTTT GTCATTTTCT | 60 |
| ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG | 120 |
| AGGCAATTAA TCCATATTTG TTTTCAATAA GGAAAAAAG ATGT | 164 |

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

| | |
|---|-----|
| ACGTAGACCA TCCAACCTTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAAACAA | 60 |
| ACTGGAGGGT ATTTATACCC AATTATCCCA TTCATTAACA TGCCCTCCTC CTCAGGCTAT | 120 |
| GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTTGT ATAAACTTCA | 180 |
| GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG | 240 |
| TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT | 300 |
| CAA | 303 |

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

| | |
|---|-----|
| ACTGCAGCTC AATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC | 60 |
| ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTGAGAGA GCTCCTTTGC CAACAGGCCCT | 120 |
| CCAAGTCAGG GCTGGGATTT GTTTCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT | 180 |
| CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGAACAAGC TGCCACTTTC TAAAGTAGCC | 240 |
| AGACTTGCCC CTGGGCCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG | 300 |
| TAGGGGTGAG CTGTGTGACT CTATGGT | 327 |

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

| | |
|--|-----|
| ACATTGTTTT TTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG | 60 |
| ACTGGAACAC ATACCCACAT CTTGTTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT | 120 |
| ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT | 173 |

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

| | |
|---|-----|
| ACAACCACTT TATCTCATCG AATTTTAAAC CCAAATCAC TCACTGTGCC TTTCTATCCT | 60 |
| ATGGGATATA TTATTTGATG CTCCATTTC AATCACAATC ATGAATAATA CACTCATACT | 120 |
| GCCCTACTAC CTGCTGCAAT AATCACAATC CCTTCCTGTC CTGACCCTGA AGCCATTGGG | 180 |
| GTGGTCCTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC | 240 |
| NCCANCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCA | 300 |
| TAGATTATNT CCAAATTCAG TCAATTAAGT TACTATTAAC ACTTACCCG ACATGTCCAG | 360 |
| CACCACTGGT AAGCCTTCTC CAGCCAACAC ACACACACAC ACACNCACAC ACACACATAT | 420 |
| CCAGGCACAG GCTACCTCAT CTTACAATC ACCCCTTTAA TTACCATGCT ATGGTG | 477 |

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

| | |
|---|-----|
| ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTTAAG AGGGAAGAAC | 60 |
| TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT | 120 |

GATGATAAAT AAGAGTCAGC CAGGTAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAACA 180
TTTCAGGCAG AGGGAACAGC AGTGAAA 207

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG 60
CACTTAAATG TGGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTTGGG T 111

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC 60
AGCAAGATGG CTTTGAAGTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT 120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG 180
GTGCATCCGG CTCAGT 196

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC 60
CTTCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACCAG 120
GAGGGAGTTT GT 132

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

| | |
|---|-----|
| ACAANACCCA NGANAGGCCA CTGGCCGTGG TGTCATGGCC TCCAAACATG AAAGTGTGAG | 60 |
| CTTCTGCTCT TATGTCCTCA TCTGACAACT CTTTACCATT TTTATCCTCG CTCAGCAGGA | 120 |
| GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGGC TTGGAGGAAG TCATCAACAC | 180 |
| CCTGGCTAGT GAGGTGCGG CGCCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA | 240 |
| GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT | 285 |

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

| | |
|---|-----|
| ACCACAGTCC TGTGGGCCA GGGCTTCATG ACCCTTCTG TGAAAAGCCA TATTATCACC | 60 |
| ACCCCAAATT TTTCTTAAA TATCTTAAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC | 120 |
| CCTAAGCCGG TTACACAGCT AACTCCCACT GGCCCTGATT TGTGAAATTG CTGCTGCCTG | 180 |
| ATTGGCACAG GAGTCGAAGG TGTTACAGCTC CCCTCCTCCG TGGAACGAGA CTCTGATTG | 240 |
| AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG | 300 |
| GTCAGGCCTG TCTCATCCAT ATGGATCTTC CGG | 333 |

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

| | |
|---|-----|
| ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAAA GATCATCAGG GCATGGATGG | 60 |
| GAAAGTGCTT TGGGAAGTGT AAAGTGCCTA ACACATGATC GATGATTTT GTTATAATAT | 120 |
| TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC | 180 |
| ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT | 240 |

GCTTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTA AGGCATGCTG 300
GCCCTGGT 308

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGAA CATATTAGGA ACTCAAATA TGAGATGATA ACAGTGCCTA 60
TTATTGATTA CTGAGAGAAC TGTTAGACAT TTAGTTGAAG ATTTTCTACA CAGGAACTGA 120
GAATAGGAGA TTATGTTTGG CCCTCATATT CTCTCCTATC CTCCTTGCCT CATTCTATGT 180
CTAATATATT CTCAATCAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT 240
AAAACCAGAT GTCTATCCTT AAGATTTTCA AATAGAAAAC AAATTAACAG ACTAT 295

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTTAA ATAGTGCTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTTCT 60
GAAGAGCAAA ACAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC 120
CTTAGT 126

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTTCTGTCTG TGTGAAAATG 60
AANCCAGCAG GCTGCCCCTA GTCAGTCCTT CTTCCAGAG AAAAAAGAGT TTGAGAAAGT 120
GCCTGGGTAA TTCACCATTA ATTTCCTCCC CCAAACCTC TGAGTCTTCC CTTAATATTT 180

100

| | |
|---|-----|
| CTGGTGGTTC TGACCAAGC AGGTCATGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA | 240 |
| NATGTTTGTA GCCTTGCATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG | 300 |
| CCAACCCTGT TTTCCAGTC CACGTAGACA GATTACAGT GCGGAATTCT GGAAGCTGGA | 360 |
| NACAGACGGG CTCTTTGCAG AGCCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG | 420 |
| TGTTCAATTCT CTGATGTCCT GT | 442 |

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

| | |
|--|-----|
| ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAACTG ATGGGTGACG TTGTAGGTTC | 60 |
| TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG | 120 |
| GCTGCTGTGG ACTGTTGTTG ATTCTCACT ACGGCCCAAG GTTGTGGAAC TGGCANAAAG | 180 |
| GTGTGTTGTT GGANTTGAGC TCGGGCGGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGGC | 240 |
| TGCTGTGGTG CCGGGANGTG AANGTGTGT GTCACTTGAG CTTGGCCAGC TCTGGAAAGT | 300 |
| ANTANATTCT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTAA | 360 |
| CGAACCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGTCTN | 420 |
| TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCNGCTGTG GAAGGTTGTA NATTGTCAAC | 480 |
| AAGGGAATAA CTTGTGGT | 498 |

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

| | |
|---|-----|
| ACCTGCATCC AGCTTCCCTG CCAAACAC AAGGAGACAT CAACCTCTAG ACAGGGAAC | 60 |
| AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT | 120 |
| GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC | 180 |
| CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCCC CATGACCCCA GATGCCTCTC | 240 |
| CCACCCTTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATT TAACATCCTG | 300 |
| GAGAAAAATG GCAGTTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAAA | 360 |
| CTTGTAGAAT GAAGCCTGGA | 380 |

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

| | |
|---|-----|
| ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA | 60 |
| CACTGTCCAC TGGCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT | 114 |

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

| | |
|---|-----|
| ACTTTCTGAA TCGAATCAAA TGATACTTAG TGTAGTTTAA ATATCCTCAT ATATATCAAA | 60 |
| GTTTTACTAC TCTGATAATT TTGTAAACCA GGTAACCAGA ACATCCAGTC ATACAGCTTT | 120 |
| TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAACTAC TCACTGT | 177 |

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

| | |
|--|-----|
| CATTTATACA GACAGGCGTG AAGACATTCA CGACAAAAC GCGAAATTCT ATCCCGTGAC | 60 |
| CANAGAAGGC AGCTACGGCT ACTCCTACAT CTGGCGTG GTGGCCTTCG CCTGCACCTT | 120 |
| CATCAGCGGC ATGATGT | 137 |

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

| | |
|---|-----|
| CTTATCACAA TGAATGTTCT CCTGGGCAGC GTTGTGATCT TTGCCACCTT CGTGACTTTA | 60 |
| TGCAATGCAT CATGCTATTT CATACTAAT GAGGGAGTTC CAGGAGATTC AACCAGGAAA | 120 |
| TGCATGGATC TCAAAGGAAA CAAACACCCA ATAACTCGG AGTGGCAGAC TGACAACTGT | 180 |
| GAGACATGCA CTTGCTACGA AACAGAAATT TCATGTTGCA CCCTTGTTTC TACACCTGTG | 240 |
| GGTTATGACA AAGACAACTG CCAAAGAATC TTCAAGAAGG AGGACTGCAA GTATATCGTG | 300 |
| GTGGAGAAGA AGGACCCAAA AAAGACCTGT TCTGTCACTG AATGGATAAT CTAATGTGCT | 360 |
| TCTAGTAGGC ACAGGGCTCC CAGGCCAGGC CTCATTCTCC TCTGGCCTCT AATAGTCAAT | 420 |
| GATTGTGTAG CCATGCCTAT CAGTAAAAAG ATNTTTGAGC AAACACTTT | 469 |

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

| | |
|---|-----|
| ACAGTTTTTT ATANATATCG ACATGCGCG CACTTGTGTT CAGTTTCATA AAGCTGGTGG | 60 |
| ATCCGCTGTC ATCCACTATT CCTTGGCTAG AGTAAAAATT ATTCTTATAG CCCATGTCCC | 120 |
| TGCAGGCCGC CCGCCCGTAG TTCTCGTTCC AGTCGTCTTG GCACACAGGG TGCCAGGACT | 180 |
| TCCTCTGAGA TGAGT | 195 |

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

| | |
|---|-----|
| ACATCTTAGT AGTGTGGCAC ATCAGGGGGC CATCAGGGTC ACAGTCACTC ATAGCCTCGC | 60 |
| CGAGGTCGGA GTCCACACCA CCGGTGTAGG TGTGCTCAAT CTTGGGCTTG GCGCCACCT | 120 |
| TTGGAGAAGG GATATGCTGC ACACACATGT CCACAAAGCC TGTGAAGTCG CCAAAGAATT | 180 |
| TTGTCAGACC AGCCTGAGCA AGGGGCGGAT GTTCAGCTTC AGTCCTCCT TCGTCAGGTG | 240 |
| GATGCCAACC TCGTCTANGG TCCGTGGGAA GCTGGTGTCC ACNTCACCTA CAACCTGGGC | 300 |
| GANGATCTTA TAAAGAGGCT CCNAGATAAA CTCACGAAA CTCTCTGCGG AGCTGCTAGT | 360 |
| NGGGGCCTTT TTGGTGAAGT TTC | 383 |

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

| | |
|---|-----|
| ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT | 60 |
| TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC | 120 |
| TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC | 180 |
| TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC | 240 |
| TGANGTC | 247 |

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

| | |
|---|-----|
| ACTTCTAAGT TTTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA | 60 |
| AATCCCTCAN CCTGTCTT CACNACTGTC TATACTGANA GTGTCATGTT TCCACAAAGG | 120 |
| GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTTCCAG TAGGGTGGGC | 180 |
| AATTCCCAAC TTCCTTGCCA CAAGCTTCCC AGGCTTTCTC CCCTGGAAAA CTCCAGCTTG | 240 |
| AGTCCCAGAT ACACTCATGG GCTGCCCTGG GCA | 273 |

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

| | |
|--|-----|
| ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC | 60 |
| AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA | 120 |
| CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTTC CACAGGTGAG | 180 |
| GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC | 240 |
| CTTGCCATGG GCAAAGGCC CTACCACAAA AACAATAGGA TCACTGCTGG GCACCAGCTC | 300 |
| ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTTCATAC ATCCAACCTGG | 360 |
| AAAGTGATCT GATACTGGAT TCTTAATTAC CTTCAAAGC TTCTGGGGGC CATCAGCTGC | 420 |
| TCGAACACTG A | 431 |

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

| | |
|---|-----|
| ACCTGTGGGC TGGGCTGTTA TGCCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC | 60 |
| TCAAGGAGCT CTGCAGGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT | 120 |
| CCCCGCTAGA AAGACACCAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTTGAT | 180 |
| GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT | 240 |
| TCAAAGCTAG GGGTCTGGCA GGTGGA | 266 |

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

| | |
|--|------|
| GGCAGCCAAA TCATAACGG CGAGGACTGC AGCCCGCACT CGCAGCCCTG GCAGGCGGCA | 60 |
| CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCGTCTTGG TGCATCCGCA GTGGGTGCTG | 120 |
| TCAGCCGCAC ACTGTTTCCA GAAGTGAGTG CAGAGCTCCT ACACCATCGG GCTGGGCCTG | 180 |
| CACAGTCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA | 240 |
| CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC | 300 |
| GAATCCGTGT CCGAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC | 360 |
| GCGGGGAAGT CTTGCCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCTACC | 420 |
| GTGCTGCAGT GCGTGAACGT GTCGGTGGTG TCTGAGGAGG TCTGCAGTAA GCTCTATGAC | 480 |
| CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GGCGGAGGGC AAGACCAGAA GGACTCCTGC | 540 |
| AACGGTGACT CTGGGGGGCC CCTGATCTGC AACCGGTACT TGCAGGGCCT TGTGTCTTTC | 600 |
| GGAAAAGCCC CGTGTGGCCA AGTTGGCGTG CCAGGTGTCT ACACCAACCT CTGCAAATTC | 660 |
| ACTGAGTGGA TAGAGAAAAC CGTCCAGGCC AGTTAACTCT GGGGACTGGG AACCCATGAA | 720 |
| CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCCTCCTCCC TCAAACCAAG GGTACAGATC | 780 |
| CCCAGCCCTC CTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCTCC TCCCTCAGAC | 840 |
| CCAGGAGTCC AGCCCTCCT CCCTCAGACC CAGGAGTCCA GACCCCCCAG CCCCTCCTCC | 900 |
| CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCCTCCCTC AGACTCAGAG GTCCAAGCCC | 960 |
| CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGGTCCCAG CCCCTCNTCC CTCAGACCCA | 1020 |
| GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTTGTTGGC ACGTTGACCC | 1080 |
| AACCTTACCA GTTGGTTTTT CATTTTTNGT CCCTTTCCCC TAGATCCAGA AATAAAGTTT | 1140 |
| AAGAGAAGNG CAAAAA AAAA AAAAAA AAAAAA AAAAAA | 1200 |
| | 1248 |

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
1           5           10           15
Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
          20           25           30
Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
          35           40           45
Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
          50           55           60
Arg Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu
65           70           75           80
Glu Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe
          85           90           95
Cys Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser
          100          105          110
Gly Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe
          115          120          125
Gly Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn
          130          135          140
Leu Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
          145          150          155

```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

GGCAGCCCCGC ACTGCAGCC CTGGCAGGCG GCACTGGTCA TGGAAAACGA ATTGTTCTGC      60
TCGGGCGTCC TGGTGCATCC GCAGTGGGTG CTGTCAGCCG CACACTGTTT CCAGAACTCC      120
TACACCATCG GGCTGGGCCT GCACAGTCTT GAGGCCGACC AAGAGCCAGG GAGCCAGATG      180
GTGGAGGCCA GCCTCTCGT ACGGCACCCA GAGTACAACA GACCCTTGCT CGCTAACGAC      240

```

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| CTCATGCTCA | TCAAGTTGGA | CGAATCCGTG | TCCGAGTCTG | ACACCATCCG | GAGCATCAGC | 300 |
| ATTGCTTCGC | AGTGCCCTAC | CGCGGGGAAC | TCTTGCCTCG | TTTCTGGCTG | GGGTCTGCTG | 360 |
| GCGAACGGTG | AGCTCACGGG | TGTGTGTCTG | CCCTCTTCAA | GGAGGTCCTC | TGCCCAGTCG | 420 |
| CGGGGGCTGA | CCAGAGCTC | TGCGTCCCAG | GCAGAATGCC | TACCGTGCTG | CAGTGCGTGA | 480 |
| ACGTGTCTGGT | GGTGTCTGAG | GAGGTCTGCA | GTAAGCTCTA | TGACCCGCTG | TACCAACCCA | 540 |
| GCATGTTCTG | CGCCGGCGGA | GGGCAAGACC | AGAAGGACTC | CTGCAACGGT | GACTCTGGGG | 600 |
| GGCCCCTGAT | CTGCAACGGG | TACTTGCAGG | GCCTTGTGTC | TTTCGGAAAA | GCCCCGTGTG | 660 |
| GCCAAGTTGG | CGTGCCAGGT | GTCTACACCA | ACCTCTGCAA | ATTCACTGAG | TGGATAGAGA | 720 |
| AAACCGTCCA | GGCCAGTTAA | CTCTGGGGAC | TGGGAACCCA | TGAAATTGAC | CCCCAAATAC | 780 |
| ATCCTGCGGA | AGGAATTCAG | GAATATCTGT | TCCCAGCCCC | TCCTCCCTCA | GGCCCAGGAG | 840 |
| TCCAGGCCCC | CAGCCCTCC | TCCCTCAAAC | CAAGGGTACA | GATCCCCAGC | CCCTCCTCCC | 900 |
| TCAGACCCAG | GAGTCCAGAC | CCCCCAGCCC | CTCCTCCCTC | AGACCCAGGA | GTCCAGCCCC | 960 |
| TCCTCCNTCA | GACCCAGGAG | TCCAGACCCC | CCAGCCCCTC | CTCCCTCAGA | CCCAGGGGTT | 1020 |
| GAGGCCCCCA | ACCCCTCCTC | CTTCAGAGTC | AGAGGTCCAA | GCCCCCAACC | CCTCGTTCCC | 1080 |
| CAGACCCAGA | GGTNNAGGTC | CCAGCCCCTC | TTCCNTCAGA | CCCAGNGGTC | CAATGCCACC | 1140 |
| TAGATTTTCC | CTGNACACAG | TGCCCCCTTG | TGGNANGTTG | ACCCAACCTT | ACCAGTTGGT | 1200 |
| TTTTCAATTT | TNGTCCCTTT | CCCCTAGATC | CAGAAATAAA | GTTTAAGAGA | NGNGCAAAAA | 1260 |
| AAAAA | | | | | | 1265 |

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| GGTCAGCCGC | AACTGTTTC | CAGAAGTGAG | TGCAGAGCTC | CTACACCATC | GGGCTGGGCC | 60 |
| TGCACAGTCT | TGAGGCCGAC | CAAGAGCCAG | GGAGCCAGAT | GGTGGAGGCC | AGCCTCTCCG | 120 |
| TACGGCACCC | AGAGTACAAC | AGACCCTTGC | TCGCTAACGA | CCTCATGCTC | ATCAAGTTGG | 180 |
| ACGAATCCGT | GTCCGAGTCT | GACACCATCC | GGAGCATCAG | CATTGCTTCG | CAGTGCCCTA | 240 |
| CCGCGGGGAA | CTCTTGCCCT | GTTTCTGGCT | GGGGTCTGCT | GGCGAACGGT | GAGCTCACGG | 300 |
| GTGTGTGTCT | GCCCTCTTCA | AGGAGGTCCT | CTGCCCAGTC | GCGGGGGCTG | ACCCAGAGCT | 360 |
| CTGCGTCCCA | GGCAGAATGC | CTACCGTGCT | GCAGTGCGTG | AACGTGTCTG | TGGTGTCTGA | 420 |
| NGAGGTCTGC | ANTAAGCTCT | ATGACCCGCT | GTACCACCCC | ANCATGTTCT | GCGCCGGCGG | 480 |
| AGGGCAAGAC | CAGAAGGACT | CCTGCAACGT | GAGAGAGGGG | AAAGGGGAGG | GCAGGCCGACT | 540 |
| CAGGGAAGGG | TGGAGAAGGG | GGAGACAGAG | ACACACAGGG | CCGCATGGCG | AGATGCAGAG | 600 |
| ATGGAGAGAC | ACACAGGGAG | ACAGTGACAA | CTAGAGAGAG | AAACTGAGAG | AAACAGAGAA | 660 |
| ATAAACACAG | GAATAAAGAG | AAGCAAAGGA | AGAGAGAAAC | AGAAACAGAC | ATGGGGAGGC | 720 |
| AGAAACACAC | ACACATAGAA | ATGCAGTTGA | CCTTCCAACA | GCATGGGGCC | TGAGGGCGGT | 780 |
| GACCTCCACC | CAATAGAAAA | TCCTCTTATA | ACTTTTGACT | CCCCAAAAAC | CTGACTAGAA | 840 |
| ATAGCCTACT | GTTGACGGGG | AGCCTTACCA | ATAACATAAA | TAGTCGATTT | ATGCATACGT | 900 |
| TTTATGCATT | CATGATATAC | CTTTGTTGGA | ATTTTGTGAT | ATTCTAAGC | TACACAGTTC | 960 |
| GTCTGTGAAT | TTTTTTAAAT | TGTTGCAACT | CTCTAAAAT | TTTTCTGATG | TGTTTATTGA | 1020 |
| AAAAATCCAA | GTATAAGTGG | ACTTGTGCAT | TCAAACCAGG | GTTGTTCAAG | GGTCAACTGT | 1080 |
| GTACCCAGAG | GGAAACAGTG | ACACAGATTC | ATAGAGGTGA | AACACGAAGA | GAAACAGGAA | 1140 |
| AAATCAAGAC | TCTACAAAGA | GGCTGGGCAG | GGTGCTCAT | GCCTGTAATC | CCAGCACTTT | 1200 |
| GGGAGGCGAG | GCAGGCAGAT | CACCTGAGGT | AAGGAGTTCA | AGACCAGCCT | GGCCAAAATG | 1260 |
| GTGAAATCCT | GTCTGTACTA | AAAATACAAA | AGTTAGCTGG | ATATGTTGGC | AGGCGCCTGT | 1320 |
| AATCCCAGCT | ACTTGGGAGG | CTGAGGCAGG | AGAATTGCTT | GAATATGGGA | GGCAGAGGTT | 1380 |
| GAAGTGAGTT | GAGATCACAC | CACTATACTC | CAGCTGGGGC | AACAGAGTAA | GACTCTGTCT | 1440 |
| CAAAAAAAAA | AAAAAAAAAA | | | | | 1459 |

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```

GCGCAGCCCT GGCAGGCGGC ACTGGTCATG GAAAACGAAT TGTTCCTGCTC GGGCGTCTCTG      60
GTGCATCCGC AGTGGGTGCT GTCAGCCGCA CACTGTTTCC AGAACTCCTA CACCATCGGG      120
CTGGGCTGAC ACAGTCTTGA GCGCGACCAA GAGCCAGGGA GCCAGATGGT GGAGGCCAGC      180
CTCTCCGTAC GGCACCCAGA GTACAACAGA CTCTTGCTCG CTAACGACCT CATGCTCATC      240
AAGTTGGACG AATCCGTGTC CGAGTCTGAC ACCATCCGGA GCATCAGCAT TGCTTCGCAG      300
TGCCCTACCG CGGGGAATCT TGCCTCGTN TCTGGCTGGG GTCTGCTGGC GAACGGCAGA      360
ATGCCTACCG TGCTGCACTG CGTGAACGTG TCGGTGGTGT CTGAGGANGT CTGCAGTAAG      420
CTCTATGACC CGCTGTACCA CCCAGCATG TTCTGCGCGG GCGGAGGGCA AGACCAGAAG      480
GACTCCTGCA ACGGTGACTC TGCGGGGGCCC CTGATCTGCA ACGGGTACTT GCAGGGCCTT      540
GTGTCTTTTC GAAAAGCCCC GTGTGGCCAA CTTGGCGTGC CAGGTGTCTA CACCAACCTC      600
TGCAAATTCA CTGAGTGGAT AGAGAAAACC GTCCAGNCCA GTTAACTCTG GGGACTGGGA      660
ACCCATGAAA TTGACCCCCA AATACATCCT GCGGAANGAA TTCAGGAATA TCTGTTCCCA      720
GCCCCCTCCT CCTCAGGCCC AGGAGTCCAG GCCCCCAGCC CCTCCTCCCT CAAACCAAGG      780
GTACAGATCC CCAGCCCCCTC CTCCCTCAGA CCCAGGAGTC CAGACCCCCC AGCCCCCTNT      840
CCNTCAGACC CAGGAGTCCA GCCCTCCTC CNTCAGACGC AGGAGTCCAG ACCCCCCAGC      900
CCNTCNTCCG TCAGACCCAG GGGTGCAGGC CCCCCAAGCC TCNTCCNTCA GAGTCAGAGG      960
TCCAAGCCCC CAACCCCTCG TTCCCCAGAC CCAGAGGTNC AGGTCCCAGC CCCTCCTCCC     1020
TCAGACCCAG CGGTCCAATG CCACCTAGAN TNTCCCTGTA CACAGTGCCC CCTTGTGGCA     1080
NGTTGACCCA ACCTTACCAG TTGGTTTTTC ATTTTTTGTC CCTTTCCCTT AGATCCAGAA     1140
ATAAAGTNTA AGAGAAGCGC AAAAAAA                      1167
  
```

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1              5              10              15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
      20              25              30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
      35              40              45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
      50              55              60
  
```

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
65 70 75 80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
85 90 95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
100 105 110

Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
115 120 125

Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
130 135 140

Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
145 150 155 160

Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
165 170 175

Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
180 185 190

Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
195 200 205

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| GCGCACTCGC | AGCCCTGGCA | GGCGGCACTG | GTCATGGAAA | ACGAATTGTT | CTGCTCGGGC | 60 |
| GTCCTGGTGC | ATCCGCAGTG | GGTGCTGTCA | GCCGCACACT | GTTTCCAGAA | CTCCTACACC | 120 |
| ATCGGGCTGG | GCCTGCACAG | TCTTGAGGCC | GACCAAGAGC | CAGGGAGCCA | GATGGTGGAG | 180 |
| GCCAGCCTCT | CCGTACGGCA | CCCAGAGTAC | AACAGACCTT | TGCTCGCTAA | CGACCTCATG | 240 |
| CTCATCAAGT | TGGACGAATC | CGTGTCGGAG | TCTGACACCA | TCCGGAGCAT | CAGCATTGCT | 300 |
| TCCGAGTGCC | CTACCGCGGG | GAACCTCTGC | CTCGTTTCTG | GCTGGGGTCT | GCTGGCGAAC | 360 |
| GATGCTGTGA | TTGCCATCCA | GTCCCAGACT | GTGGGAGGCT | GGGAGTGTGA | GAAGCTTTCC | 420 |
| CAACCCTGGC | AGGGTTGTAC | CATTTCGGCA | ACTTCCAGTG | CAAGGACGTC | CTGCTGCATC | 480 |
| CTCACTGGGT | GCTCACTACT | GCTCACTGCA | TCACCCGGAA | CACTGTGATC | AAC TAGCCAG | 540 |
| CACCATAGTT | CTCCGAAGTC | AGACTATCAT | GATTACTGTG | TTGACTGTGC | TGTCTATTGT | 600 |
| ACTAACCATG | CCGATGTTTA | GGTGAAATTA | GCGTCACTTG | GCCTCAACCA | TCTTGGTATC | 660 |
| CAGTTATCCT | CACTGAATTG | AGATTTCCTG | CTTCAGTGTC | AGCCATTCCC | ACATAATTTT | 720 |
| TGACCTACAG | AGGTGAGGGA | TCATATAGCT | CTTCAAGGAT | GCTGGTACTC | CCCTCACAAA | 780 |
| TTCATTTTCT | CTGTTGTAGT | GAAAGGTGCG | CCCTCTGGAG | CCTCCAGGG | TGGGTGTGCA | 840 |
| GGTCACAATG | ATGAATGTAT | GATCGTGTTC | CCATTACCCA | AAGCCTTTAA | ATCCCTCATG | 900 |
| CTCAGTACAC | CAGGGCAGGT | CTAGCATTTT | TTCATTTAGT | GTATGCTGTC | CATTCATGCA | 960 |
| ACCACCTCAG | GACTCCTGGA | TTCTCTGCCT | AGTTGAGCTC | CTGCATGCTG | CCTCCTTGGG | 1020 |
| GAGGTGAGGG | AGAGGGCCCA | TGTTTCAATG | GGATCTGTGC | AGTTGTAACA | CATTAGGTGC | 1080 |

TTAATAAACA GAAGCTGTGA TGTAAAAAA AAAAAAAA

1119

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1             5             10             15

Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
      20             25             30

Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
      35             40             45

Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
      50             55             60

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
      65             70             75             80

Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
      85             90             95

Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
      100            105            110

Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
      115            120            125

Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
      130            135            140

Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
      145            150            155            160

Pro Gly Thr Leu

```

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT

60

110

| | |
|---|-----|
| CCAGCTGCCC CCGGCCGGGG GATGCGAGGC TCGGAGCACC CTTGCCCGGC TGTGATTGCT | 120 |
| GCCAGGCACT GTTCATCTCA GCTTTTCTGT CCCTTTGCTC CCGGCAAGCG CTTCTGCTGA | 180 |
| AAGTTCATAT CTGGAGCCTG ATGTCTTAAC GAATAAAGGT CCCATGCTCC ACCCGAAAAA | 240 |
| AAAAAAAAAA | 250 |

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

| | |
|--|-----|
| ACTAGTCCAG TGTGGTGGA TCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAACA | 60 |
| TCACCCAGAC CCCGCCCTG CCCGTGCCC ACGTGCTGC TAACGACAGT ATGATGCTTA | 120 |
| CTCTGCTACT CGGAACTAT TTTTATGTAA TTAATGTATG CTTTCTTGTT TATAAATGCC | 180 |
| TGATTTAAAA AAAAAAAAAA AA | 202 |

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

| | |
|---|-----|
| TCCYTTTGKT NAGGTTTKKG AGACAMCCCK AGACCTWAAN CTGTGTCACA GACTTCYNGG | 60 |
| AATGTTTAGG CAGTGCTAGT AATTCYTCG TAATGATTCT GTTATTACTT TCCTNATTCT | 120 |
| TTATTCCTCT TTCTCTGAA GATTAATGAA GTTGAAAATT GAGGTGGATA AATACAAAAA | 180 |
| GGTAGTGTGA TAGTATAAGT ATCTAAGTGC AGATGAAAGT GTGTTATATA TATCCATTCA | 240 |
| AAATTATGCA AGTTAGTAAT TACTCAGGGT TAACTAAATT ACTTTAATAT GCTGTTGAAC | 300 |
| CTACTCTGTT CCTTGGCTAG AAAAAATTAT AAACAGGACT TTGTTAGTTT GCGAAGCCAA | 360 |
| ATTGATAATA TTCTATGTC TAAAAGTTGG GCTATACATA AATTATTAAG AAATATGGAW | 420 |
| TTTTATTCCC AGGAATATGG KGTTCATTTT ATGAATATTA CSCRGGATAG AWGTWTGAGT | 480 |
| AAAAYCAGTT TTGGTWAATA YGTWAATATG TCMTAAATAA ACAAKGCTTT GACTTATTTT | 540 |
| CAAAAAAAAA AAAAAAAA | 558 |

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

| | |
|---|-----|
| ACAGGGWTTK GRGGATGCTA AGSCCCCRGA RWTYGTTTGA TCCAACCCTG GCTTWTTTTC | 60 |
| AGAGGGGAAA ATGGGGCCTA GAAGTTACAG MSCATYTAGY TGGTGCGMTG GCACCCCTGG | 120 |
| CSTCACACAG ASTCCCGAGT AGCTGGGACT ACAGGCACAC AGTCACTGAA GCAGGCCCTG | 180 |
| TTWGCAATTC ACGTTGCCAC CTCCAACCTA AACATTCTTC ATATGTGATG TCCTTAGTCA | 240 |
| CTAAGGTTAA ACTTTCCAC CCAGAAAAGG CAACCTAGAT AAAATCTTAG AGTACTTTCA | 300 |
| TACTMTTCTA AGTCCTCTTC CAGCCTCACT KKGAGTCCTM CYTGGGGGTT GATAGGAANT | 360 |
| NTCTCTTGGC TTTCTCAATA AARTCTCTAT YCATCTCATG TTTAATTGTT TACGCATARA | 420 |

AWTGSTGARA AAATTAAAAT GTTCTGGTTY MACTTTAAAA ARAAAAAAAAA AAAAAAAAAA 479

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGGCGGGAGC | AGAAGCTAAA | GCCAAAGCCC | AAGAAGAGTG | GCAGTGCCAG | CACTGGTGCC | 60 |
| AGTACCACTA | CCAATAACAG | TGCCAGTGCC | AGTGCCAGCA | CCAGTGGTGG | CTTCAGTGCT | 120 |
| GGTGCCAGCC | TGACCGCCAC | TCTCACATTT | GGGCTCTTCG | CTGGCCTTGG | TGGAGCTGGT | 180 |
| GCCAGCACCA | GTGGCAGCTC | TGGTGCCTGT | GGTTTCTCCT | ACAAGTGAGA | TTTtagatat | 240 |
| TGTTAATCCT | GCCAGTCTTT | CTCTTCAAGC | CAGGGTGCAT | CCTCAGAAAC | CTACTCAACA | 300 |
| CAGCACTCTA | GGCAGCCACT | ATCAATCAAT | TGAAGTTGAC | ACTCTGCATT | ARATCTATTT | 360 |
| GCCATTTCAA | AAAAAAAAAA | AAAA | | | | 384 |

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACCGAATTGG | GACCGCTGGC | TTATAAGCGA | TCATGTYINT | CCRGATKAC | CTCAACGAGC | 60 |
| AGGGAGATCG | AGTCTATACG | CTGAAGAAAT | TTGACCCGAT | GGGACAACAG | ACCTGCTCAG | 120 |
| CCCATCCTGC | TCGGTTCTCC | CCAGATGACA | AATACTCTSG | ACACCGAATC | ACCATCAAGA | 180 |
| AACGCTTCAA | GGTGCTCATG | ACCCAGCAAC | CGCGCCCTGT | CCTCTGAGGG | TCCCTTAAAC | 240 |
| TGATGTCTTT | TCTGCCACCT | GTTACCCCTC | GGAGACTCCG | TAACCAAAC | CTTCGGACTG | 300 |
| TGAGCCCTGA | TGCCTTTTTC | CCAGCCATAC | TCTTTGGCAT | CCAGTCTCTC | GTGGCGATTG | 360 |
| ATTATGCTTG | TGTGAGGCAA | TCATGGTGGC | ATCACCCATA | AAGGGAACAC | ATTTGACTTT | 420 |
| TTTTTCTCAT | ATTTTAAATT | ACTACMAGAW | TATTWMAGAW | WAAATGAWTT | GAAAACTST | 480 |
| TAAAAAAAAA | AAAAAA | | | | | 496 |

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCTGGTAGCC | TATGGCGKGG | CCCACGGAGG | GGCTCCTGAG | GCCACGGRAC | AGTGAATTCC | 60 |
| CAAGTATCYT | GCGCSGCGTC | TTCTACCGTC | CCTACCTGCA | GATCTTCGGG | CAGATTCCCC | 120 |
| AGGAGGACAT | GGACGTGGCC | CTCATGGAGC | ACAGCAACTG | YTCGTGGGAG | CCCGGCTTCT | 180 |
| GGGCACACCC | TCCTGGGGCC | CAGGCGGGCA | CCTGCGTCTC | CCAGTATGCC | AACTGGCTGG | 240 |
| TGGTGCTGCT | CCTCGTCATC | TTCTGCTCG | TGGCCAACAT | CCTGCTGGTC | AACTTGCTCA | 300 |
| TTGCCATGTT | CAGTTACACA | TTCGGCAAAG | TACAGGGCAA | CAGCGATCTC | TACTGGGAAG | 360 |
| GCGCAGCGTT | ACCGCCTCAT | CCGG | | | | 384 |

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 577 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAGTTAGCTC | CTCCACAACC | TTGATGAGGT | CGTCTGCAGT | GGCCTCTCGC | TTCATACCGC | 60 |
| TNCCATCGTC | ATACTGTAGG | TTTGCCACCA | CYTCCTGGCA | TCTTGGGGCG | GCNTAATATT | 120 |
| CCAGGAAACT | CTCAATCAAG | TCACCGTCGA | TGAAACCTGT | GGGCTGGTTC | TGTCTTCCGC | 180 |
| TCGGTGTGAA | AGGATCTCCC | AGAAGGAGTG | CTCGATCTTC | CCCACACTTT | TGATGACTTT | 240 |
| ATTGAGTCGA | TTCTGCATGT | CCAGCAGGAG | GTTGTACCAG | CTCTCTGACA | GTGAGGTCAC | 300 |
| CAGCCCTATC | ATGCCGTTGA | MCGTGCCGAA | GARCACCGAG | CCTTGTGTGG | GGGKKGAAGT | 360 |
| CTCACCAGAG | TTCTGCATTA | CCAGAGAGCC | GTGGCAAAAG | ACATTGACAA | ACTCGCCCAG | 420 |
| GTGGAAGAA | AMCAMCTCCT | GGARGTGCTN | GCCGCTCCTC | GTCMGTGGT | GGCAGCGCTW | 480 |
| TCCTTTTGAC | ACACAAACAA | GTAAAGGCA | TTTTCAGCCC | CCAGAAANTT | GTCATCATCC | 540 |
| AAGATNTCGC | ACAGCACTNA | TCCAGTTGGG | ATTAAAT | | | 577 |

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|-----|
| AACATCTTCC | TGTATAATGC | TGTGTAATAT | CGATCCGATN | TTGTCTGSTG | AGAATYCATW | 60 |
| ACTKGGAAAA | GMAACATTAA | AGCCTGGACA | CTGGTATTAA | AATTCACAAT | ATGCAACACT | 120 |
| TTAAACAGTG | TGTCAATCTG | CTCCCYYNAC | TTTGTCTATCA | CCAGTCTGGG | AAKAAGGGTA | 180 |
| TGCCCTATTTC | ACACCTGTTA | AAAGGGCGCT | AAGCATTTTT | GATTCAACAT | CTTTTTTTTT | 240 |
| GACACAAGTC | CGAAAAAAGC | AAAAGTAAAC | AGTTATYAAT | TTGTTAGCCA | ATTCACITTC | 300 |
| TTTCATGGGAC | AGAGCCATYT | GATTTAAAAA | GCAAATTGCA | TAATATTGAG | CTTYGGGAGC | 360 |
| TGATATTTGA | GCGGAAGAGT | AGCCTTTCTA | CTTCACCAGA | CACAACTCCC | TTTCATATTG | 420 |
| GGATGTTNAC | NAAAGTWATG | TCTCTWACAG | ATGGGATGCT | TTTGTGGCAA | TTCTGTTCTG | 480 |
| AGGATCTCCC | AGTTTATTTA | CACTTGACAC | AAGAAGGCGT | TTCTTCCTC | AGGC | 534 |

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGAAACCACT | ATCTCTNAAA | ACAACCTCTC | ATACCTTGTG | GACCTAATTT | TGTGTGCGTG | 60 |
| TGTGTGTGCG | CGCATATTAT | ATAGACAGGC | ACATCTTTTT | TACTTTTGTA | AAAGCTTATG | 120 |
| CCTCTTTGGT | ATCTATATCT | GTGAAAGTTT | TAATGATCTG | CCATAATGTC | TTGGGGACCT | 180 |
| TTGTCTTCTG | TGTAAATGGT | ACTAGAGAAA | ACACCTATNT | TATGAGTCAA | TCTAGTTNGT | 240 |
| TTTATTCGAC | ATGAAGGAAA | TTTCCAGATN | ACAACACTNA | CAAACTCTCC | CTKGACKARG | 300 |
| GGGGACAAAG | AAAAGCAAAA | CTGAMCATAA | RAACAATWA | CCTGGTGAGA | ARTTGCATAA | 360 |
| ACAGAAATWR | GGTAGTATAT | TGAARNACAG | CATCATTAAT | RMGTTWTKTT | WTTCTCCCTT | 420 |

| | | | | | | |
|-------------|-------------|------------|------------|------------|------------|-----|
| GCAAAAAACA | TGTACNGACT | TCCCGTTGAG | TAATGCCAAG | TTGTTTTTTT | TATNATAAAA | 480 |
| CTTGCCCTTC | ATTACATGTT | TNAAAGTGGT | GTGGTGGGCC | AAAATATTGA | AATGATGGAA | 540 |
| CTGACTGATA | AAGCTGTACA | AATAAGCAGT | GTGCCTAACA | AGCAACACAG | TAATGTTGAC | 600 |
| ATGCTTAATT | CACAAATGCT | AATTTTATTA | TAAATGTTTG | CTAAAATACA | CTTTGAACTA | 660 |
| TTTTTCTGTN | TTCCCGAGAGC | TGAGATNTTA | GATTTTATGT | AGTATNAAGT | GAAAAANTAC | 720 |
| GAAAAATAATA | ACATTGAAGA | AAAANANAAA | AAANAAAAAA | A | | 761 |

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTGCCGATN | CTACTATTTT | ATTGCAGGAN | GTGGGGGTGT | ATGCACCGCA | 60 |
| CACCGGGGCT | ATNAGAAGCA | AGAAGGAAGG | AGGGAGGGCA | CAGCCCCTTG | CTGAGCAACA | 120 |
| AAGCCGCTTG | CTGCCTTCTC | TGTCTGTCTC | CTGGTGCAGG | CACATGGGGA | GACCTTCCCC | 180 |
| AAGGCAGGGG | CCACCAGTCC | AGGGGTGGGA | ATACAGGGGG | TGGGANGTGT | GCATAAGAAG | 240 |
| TGATAGGCAC | AGGCCACCCG | GTACAGACCC | CTCGGCTCCT | GACAGGTNGA | TTTCGACCAG | 300 |
| GTCATTGTGC | CCTGCCCAGG | CACAGCGTAN | ATCTGGAAAA | GACAGAATGC | TTTCCTTTTC | 360 |
| AAATTTGGCT | NGTCATNGAA | NGGGCANTTT | TCCAANTTNG | GCTNGGTCTT | GGTACNCTTG | 420 |
| GTTCGGCCCA | GCTCCNCGTC | CAAAAANTAT | TCACCCNNCT | CCNAATTGCT | TGCNGGNCCC | 480 |
| CC | | | | | | 482 |

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

| | | | | | | |
|-------------|------------|-------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTAAACA | GTTTTTCACA | ACAAAATTTA | TTAGAAGAAT | AGTGGTTTTG | 60 |
| AAAACCTCTCG | CATCCAGTGA | GAACCTACCAT | ACACCACATT | ACAGCTNGGA | ATGTNCTCCA | 120 |
| AATGTCTGGT | CAAATGATAC | AATGGAACCA | TTCAATCTTA | CACATGCACG | AAAGAACAAG | 180 |
| CGCTTTTGAC | ATACAATGCA | CAAAAAAAAA | AGGGGGGGGG | GACCACATGG | ATTAAAATTT | 240 |
| TAAGTACTCA | TCACATACAT | TAAGACACAG | TTCTAGTCCA | GTGNAAAATC | AGAACTGCNT | 300 |
| TGAAAAATTT | CATGTATGCA | ATCCAACCAA | AGAACTTNAT | TGGTGATCAT | GANTNCTCTA | 360 |
| CTACATCNAC | CTTGATCATT | GCCAGGAACN | AAAAGTTNAA | ANCACNCNGT | ACAAAAANAA | 420 |
| TCTGTAATTN | ANTTCAACCT | CCGTACNGAA | AAATNTTNTT | TATACACTCC | C | 471 |

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GAGGGATTGA | AGGTCTGTTC | TASTGTCGGM | CTGTTTCAGCC | ACCAACTCTA | ACAAGTTGCT | 60 |
| GTCTTCCACT | CACTGTCTGT | AAGCTTTTTA | ACCCAGACWG | TATCTTCATA | AATAGAACAA | 120 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATTCTTCACC | AGTCACATCT | TCTAGGACCT | TTTTGGATTG | AGTTAGTATA | AGCTCTTCCA | 180 |
| CTTCCTTTGT | TAAGACTTCA | TCTGGTAAAG | TCTTAAGTTT | TGTAGAAAGG | AATTYAATTG | 240 |
| CTCGTTCTCT | AACAATGTCC | TCTCCTTGAA | GTATTTGGCT | GAACAACCCA | CCTAAAGTCC | 300 |
| CTTTGTGCAT | CCATTTTAAA | TATACTTAAT | AGGGCATTGK | TNCACTAGGT | TAAATTCTGC | 360 |
| AAGAGTCATC | TGTCTGCAA | AGTTGCGTTA | GTATATCTGC | CA | | 402 |

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GAGCTCGGAT | CCAATAATCT | TTGTCTGAGG | GCAGCACACA | TATNCAGTGC | CATGGNAACT | 60 |
| GGTCTACCCC | ACATGGGAGC | AGCATGCCGT | AGNTATATAA | GGTCATTCCC | TGAGTCAGAC | 120 |
| ATGCYTYTTT | GAYTACCGTG | TGCCAAGTGC | TGGTGATTCT | YAACACACYT | CCATCCCGYT | 180 |
| CTTTTGTGGA | AAAAGTGGCA | CTTKTCTGGA | ACTAGCARGA | CATCACTTAC | AAATTCACCC | 240 |
| ACGAGACACT | TGAAAGGTGT | AACAAAGCGA | YTCTTGCAAT | GCTTTTGTGC | CCTCCGGCAC | 300 |
| CAGTTGTCAA | TACTAACCCG | CTGGTTTGCC | TCCATCACAT | TTGTGATCTG | TAGCTCTGGA | 360 |
| TACATCTCCT | GACAGTACTG | AAGAACTTCT | TCTTTTGTTC | CAAAAGCARG | TCTTGGTGCC | 420 |
| TGTTGGATCA | GGTTCCCATT | TCCCAGTCYG | AATGTTTACA | TGGCATATTT | WACTTCCCAC | 480 |
| AAAACATTGC | GATTTGAGGC | TCAGCAACAG | CAAATCCTGT | TCCGGCATTG | GCTGCAAGAG | 540 |
| CCTCGATGTA | GCCGCGCCAGC | GCCAAGGCAG | GCGCCGTGAG | CCCCACCAGC | AGCAGAAGCA | 600 |
| G | | | | | | 601 |

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATACAGCCCA | NATCCCACCA | CGAAGATGCG | CTTGTTGACT | GAGAACCTGA | TGCGGTCACT | 60 |
| GGTCCCGCTG | TAGCCCCAGC | GACTCTCCAC | CTGCTGGAAG | CGTTTGATGC | TGCACTCYTT | 120 |
| CCCAACGCAG | GCAGMAGCGG | GSCCGGTCAA | TGAACTCCAY | TCGTGGCTTG | GGGTKGACGG | 180 |
| TKAAGTGACG | GAAGAGGCTG | ACCACCTCGC | GGTCCACCAG | GATGCCCGAC | TGTGCGGGAC | 240 |
| CTGCAGCGAA | ACTCCTCGAT | GGTCATGAGC | GGGAAGCGAA | TGAGGCCAG | GGCCTTGCCC | 300 |
| AGAACCTTCC | GCCTGTTCTC | TGGCGTCACC | TGCAGCTGCT | GCCGCTGACA | CTCGGCCTCG | 360 |
| GACCAGCGGA | CAAACGGCRT | TGAACAGCCG | CACCTCACGG | ATGCCAGTG | TGTGCGGCTC | 420 |
| CAGGAMMGS | ACCAGCGTGT | CCAGGTCAAT | GTGCGTGAAG | CCCTCCGCGG | GTRATGGCGT | 480 |
| CTGCAGTGTT | TTGTGCGATG | TTCTCCAGGC | ACAGGCTGGC | CAGCTGCGGT | TCATCGAAGA | 540 |
| GTCGCGCCTG | CGTGAGCAGC | ATGAAGGCGT | TGTGCGCTCG | CAGTTCTTCT | TCAGGAAGTC | 600 |
| CACGCAAT | | | | | | 608 |

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

| | | | | | | |
|------------|-------------|-------------|------------|------------|------------|-----|
| GAACGGCTGG | ACCTTGCCCTC | GCATTGTGCT | TGCTGGCAGG | GAATACCTTG | GCAAGCAGYT | 60 |
| CCAGTCCGAG | CAGCCCCAGA | CCGCTGCCGC | CCGAAGCTAA | GCCTGCCTCT | GGCCTTCCCC | 120 |
| TCCGCCTCAA | TGCAGAACCA | GTAAGTGGGAG | CACTGTGTTT | AGAGTTAAGA | GTGAACACTG | 180 |
| TTTGATTTTA | CTTGGGAATT | TCCTCTGTTA | TATAGCTTTT | CCCAATGCTA | ATTTCCAAAC | 240 |
| AACAACAACA | AAATAACATG | TTTGCCTGTT | AAGTTGTATA | AAAGTAGGTG | ATTCTGTATT | 300 |
| TAAAGAAAAT | ATTACTGTTA | CATATACTGC | TTGCAATTTT | TGTATTTATT | GKTNCTSTGG | 360 |
| AAATAAATAT | AGTTATTAAA | GGTTGTCANT | CC | | | 392 |

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCSTTKGAGG | GGTKAGGKYC | CAGTTYCCGA | GTGGAAGAAA | CAGGCCAGGA | GAAGTGCCTG | 60 |
| CCGAGCTGAG | GCAGATGTTT | CCACAGTGAC | CCCCAGAGCC | STGGGSTAT | GTCTCTGACC | 120 |
| CCTCNCAAGG | AAAGACCACS | TTCTGGGGAC | ATGGGCTGGA | GGGCAGGACC | TAGAGGCACC | 180 |
| AAGGGAAGGC | CCCATTCGGG | GGSTGTTCCT | CGAGGAGGAA | GGGAAGGGGC | TCTGTGTGCC | 240 |
| CCCCASGAGG | AAGAGGCCCT | GAGTCCTGGG | ATCAGACACC | CCTTCACGTG | TATCCCCACA | 300 |
| CAAATGCAAG | CTCACCAAGG | TCCCCTCTCA | GTCCCCTTCC | STACACCCTG | AMCGGCCACT | 360 |
| GSCSCACACC | CACCCAGAGC | ACGCCACCCG | CCATGGGGAR | TGTGCTCAAG | GARTCGCNGG | 420 |
| GCARCGTGGA | CATCTNGTCC | CAGAAGGGGG | CAGAATCTCC | AATAGANGGA | CTGARCMSTT | 480 |
| GCTNANAAAA | AAAAANAAAA | AA | | | | 502 |

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGTTACTTGG | TTTCATTGCC | ACCACTTAGT | GGATGTCATT | TAGAACCATT | TTGTCTGCTC | 60 |
| CCTCTGGAAG | CCTTGCGCAG | AGCGGACTTT | GTAATTGTTG | GAGAATAACT | GCTGAATTTT | 120 |
| WAGCTGTTTK | GAGTTGATTS | GCACCACTGC | ACCCACAAC | TCAATATGAA | AACYAWTTGA | 180 |
| ACTWATTTAT | TATCTTGTGA | AAAGTATAAC | AATGAAAATT | TTGTTCATAC | TGTATTKATC | 240 |
| AAGTATGATG | AAAAGCAAWA | GATATATATT | CTTTTATTAT | GTTAAATTAT | GATTGCCATT | 300 |
| ATTAATCGGC | AAAATGTGGA | GTGTATGTTT | TTTTCACAGT | AATATATGCC | TTTTGTAACT | 360 |
| TCACTTGGTT | ATTTTATTGT | AAATGARTTA | CAAAATTCTT | AATTTAAGAR | AATGGTATGT | 420 |
| WATATTTATT | TCATTAATTT | CTTTCCTKGT | TTACGTWAAT | TTTGAAAAGA | WTGCATGATT | 480 |
| TCTTGACAGA | AATCGATCTT | GATGCTGTGG | AAGTAGTTTG | ACCCACATCC | CTATGAGTTT | 540 |
| TTCTTAGAAT | GTATAAAGGT | TGTAGCCCAT | CNAACTTCAA | AGAAAAAAT | GACCACATAC | 600 |
| TTTGCAATCA | GGCTGAAATG | TGGCATGCTN | TTCTAATTCC | AACTTTATAA | ACTAGCAAAN | 660 |
| AAGTG | | | | | | 665 |

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| TTTNTTTTTT | TTTTTTTTGC | AGGAAGGATT | CCATTATTGG | TGGATGCATT | TTCACAATAT | 60 |
| ATGTTTATTG | GAGCGATCCA | TTATCAGTGA | AAAGTATCAA | GTGTTTATAA | NATTTTTAGG | 120 |
| AAGGCAGATT | CACAGAACAT | GCTNGTCNGC | TTGCAGTTTT | ACCTCGTANA | GATNACAGAG | 180 |
| AATTATAGTC | NAACCAGTAA | ACNAGGAATT | TACTTTTCAA | AAGATTAAAT | CCAAACTGAA | 240 |
| CAAAATTCTA | CCCTGAAACT | TACTCCATCC | AAATATTGGA | ATAANAGTCA | GCAGTGATAC | 300 |
| ATTCTCTTCT | GAACTTTAGA | TTTTCTAGAA | AAATATGTAA | TAGTGATCAG | GAAGAGCTCT | 360 |
| TGTTCAAAAG | TACAACNAAG | CAATGTTCCC | TTACCATAGG | CCTTAATTCA | AACTTTGATC | 420 |
| CATTTCACTC | CCATCACGGG | AGTCAATGCT | ACCTGGGACA | CTTGTATTTT | GTTTCATNCTG | 480 |
| ANCNTGGCTT | AA | | | | | 492 |

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTNTTTTGN | ATTTCACTCT | GTANNAANTA | TTTTCATTAT | GTTTATTANA | AAAATATNAA | 60 |
| TGTNTCCACN | ACAAATCATN | TTACNTNAGT | AAGAGGCCAN | CTACATTGTA | CAACATACAC | 120 |
| TGAGTATATT | TTGAAAAGGA | CAAGTTTAAA | GTANACNCAT | ATTGCCGANC | ATANCACATT | 180 |
| TATACATGGC | TTGATTGATA | TTAGCACAG | CANAACTGA | GTGAGTTACC | AGAAANAAAT | 240 |
| NATATATGTC | AATCNGATTT | AAGATACAAA | ACAGATCCTA | TGGTACATAN | CATCNTGTAG | 300 |
| GAGTTGTGGC | TTTATGTTTA | CTGAAAGTCA | ATGCAGTTCC | TGTACAAAGA | GATGGCCGTA | 360 |
| AGCATTCTAG | TACCTCTACT | CCATGGTTAA | GAATCGTACA | CTTATGTTTA | CATATGTNCA | 420 |
| GGGTAAGAAT | TGTGTTAAGT | NAANTTATGG | AGAGGTCCAN | GAGAAAAATT | TGATNCAA | 478 |

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| AGTGACTTGT | CCTCCAACAA | AACCCCTTGA | TCAAGTTTGT | GGCACTGACA | ATCAGACCTA | 60 |
| TGCTAGTTCC | TGTCATCTAT | TCGCTACTAA | ATGCAGACTG | GAGGGGACCA | AAAAGGGGCA | 120 |
| TCAACTCCAG | CTGGATTATT | TTGGAGCCTG | CAAATCTATT | CCTACTTGTA | CGGACTTTGA | 180 |
| AGTGATTTCAG | TTTCCTCTAC | GGATGAGAGA | CTGGCTCAAG | AATATCCTCA | TGCAGCTTTA | 240 |
| TGAAGCCNAC | TCTGAACACG | CTGTTTATCT | NAGATGAGAA | NCAGAGAAAT | AAAGTCNAGA | 300 |
| AAATTTACCT | GGANGAAAAG | AGGCTTTNGG | CTGGGGACCA | TCCCATTGAA | CCTTCTCTTA | 360 |
| ANGGACTTTA | AGAANAAACT | ACCACATGTN | TGTNGTATCC | TGGTGCCNGG | CCGTTTANTG | 420 |
| AACNTNGACN | NCACCCTTNT | GGAATANANT | CTTGACNGCN | TCCTGAACCT | GCTCCTCTGC | 480 |
| GA | | | | | | 482 |

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

| | |
|---|-----|
| CGGCCGCAAG TGCAACTCCA GCTGGGGCCG TGCGGACGAA GATTCTGCCA GCAGTTGGTC | 60 |
| CGACTGCGAC GACGGCGGCG GCGACAGTCG CAGGTGCAGC GCGGGCGCCT GGGGTCTTGC | 120 |
| AAGGCTGAGC TGACGCCGCA GAGGTCGTGT CACGTCCCAC GACCTTGACG CCGTCGGGGA | 180 |
| CAGCCGGAAC AGAGCCCGGT GAANGCGGA GGCCTCGGG AGCCCCCTCG GAAGGGCGGG | 240 |
| CCGAGAGATA CGCAGGTGCA GGTGCGGCC | 270 |

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

| | |
|--|-----|
| TTTTTTTTTT TTTTGAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTTGCA | 60 |
| GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTCAG GTCAACTTCC TTTGTCGTGG | 120 |
| TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGG AAANCGAAGC ANAANTAACA | 180 |
| TGGAGTGGGT GCACCCCTCCC TGTAGAACCT GGTTACNAAA GCTTGGGGCA GTTCACCTGG | 240 |
| TCTGTGACCG TCATTTTCTT GACATCAATG TTATTAGAAG TCAGGATATC TTTTAGAGAG | 300 |
| TCCACTGTNT CTGGAGGGAG ATTAGGGTTT CTTGCCAANA TCCAANCAAA ATCCACNTGA | 360 |
| AAAAGTTGGA TGATNCANGT ACNGAATACC GANGGCATAN TTCTCATANT CGGTGGCCA | 419 |

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

| | |
|--|-----|
| TTTNTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT | 60 |
| TGGCACTTAA TCCATTTTAA TTTCAAAATG TCTACAAANT TTNAATNCNC CATTATACNG | 120 |
| GTNATTTTNC AAAATCTAAA NNTTATTCAA ATNTNAGCCA AANTCCTTAC NCAATNNAA | 180 |
| TACNCNCAAA AATCAAAAAT ATACNTNTCT TTCAGCAAAAC TTNGTTACAT AAATTAAAAA | 240 |
| AATATATACG GCTGGTGTTC TCAAAGTACA ATTATCTTAA CACTGCAAAC ATNTTTNNAA | 300 |
| GGAACATAAA TAAAAAATAA CACTNCCGCA AAGGTAAAG GGAACAACAA ATTCNTTTTA | 360 |
| CAACANCNC NATTATAAAA ATCATATCTC AAATCTTAGG GGAATATATA CTTACACNG | 420 |
| GGATCTTAAC TTTTACTNCA CTTTGTATAT TTTTTTANAA CCATTGTNTT GGGCCCAACA | 480 |
| CAATGGNAAT NCCNCCNCNC TGGACTAGT | 509 |

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| TTTTTTTTTT | TTTTTTTTGA | CCCCCTCTT | ATAAAAACA | AGTTACCATT | TTATTTTACT | 60 |
| TACACATATT | TATTTTATAA | TTGGTATTAG | ATATTCAAAA | GGCAGCTTTT | AAAATCAAAC | 120 |
| TAAATGGAAA | CTGCCTTAGA | TACATAATTC | TTAGGAATTA | GCTTAAAATC | TGCCTAAAAGT | 180 |
| GAAAATCTTC | TCTAGCTCTT | TTGACTGTAA | ATTTTGTGACT | CTTGTA AAC | ATCCAAATTC | 240 |
| ATTTTCTTG | TCTTAAAAT | TATCTAATCT | TTCCATTTTT | TCCCTATTCC | AAGTCAATTT | 300 |
| GCTTCTCTAG | CCTCATTTCC | TAGCTCTTAT | CTACTATTAG | TAAGTGGCTT | TTTCCTAAA | 360 |
| AGGGAACA | GGAAGAGANA | ATGGCACACA | AAACAAACAT | TTTATATTCA | TATTTCTACC | 420 |
| TACGTTAATA | AAATAGCATT | TTGTGAAGCC | AGCTCAAAAG | AAGGCTTAGA | TCCTTTTATG | 480 |
| TCCATTTTAG | TCATAAACG | ATATCNAAAG | TGCCAGAATG | CAAAGGTTT | GTGAACATTT | 540 |
| ATTCAAAAGC | TAATATAAGA | TATTTACAT | ACTCATCTTT | CTG | | 583 |

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTNT | TTTTTTTTTT | TTTTTNTCTC | TTCTTTTTTT | TTGANAATGA | GGATCGAGTT | 60 |
| TTTCACTCTC | TAGATAGGGC | ATGAAGAAAA | CTCATCTTTC | CAGCTTTAAA | ATAACAATCA | 120 |
| AATCTCTTAT | GCTATATCAT | ATTTTAAGTT | AACTAATGA | GTCAGTGGCT | TATCTTCTCC | 180 |
| TGAAGGAAAT | CTGTTTCATC | TTCTCATTCA | TATAGTTATA | TCAAGTACTA | CCTTGATAT | 240 |
| TGAGAGGTTT | TTCTTCTCTA | TTTACACATA | TATTTCCATG | TGAATTGTGA | TCAAACCTTT | 300 |
| ATTTTCATGC | AAACTAGAAA | ATAATGTNTT | CTTTTGCATA | AGAGAAGAGA | ACAATATNAG | 360 |
| CATTACAAAA | CTGCTCAAAT | TGTTTGTTAA | GNTTATCCAT | TATAATTAGT | TNGGCAGGAG | 420 |
| CTAATACAAA | TCACATTTAC | NGACNAGCAA | TAATAAACT | GAAGTACCAG | TTAAATATCC | 480 |
| AAAATAATTA | AAGGAACATT | TTAGCCTGG | GTATAATTAG | CTAATTCAT | TTACAAGCAT | 540 |
| TTATTNAGAA | TGAATTCACA | TGTTATTATT | CCNTAGCCCA | ACACAATGG | | 589 |

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTNTTTTT | TTTTTTCAGT | AATAATCAGA | ACAATATTTA | TTTTTATATT | TAAAATTCAT | 60 |
| AGAAAAGTGC | CTTACATTTA | ATAAAAGTTT | GTTTCTCAAA | GTGATCAGAG | GAATTAGATA | 120 |
| TNGTCTTGAA | CACCAATATT | AATTTGAGGA | AAATACACCA | AAATACATTA | AGTAAATTAT | 180 |
| TTAAGATCAT | AGAGCTTGTA | AGTGAAAAGA | TAAAATTGTA | CCTCAGAAAC | TCTGAGCATT | 240 |
| AAAAATCCAC | TATTAGCAAA | TAAATTACTA | TGGACTTCTT | GCTTTAATTT | TGTGATGAAT | 300 |
| ATGGGGTGTC | ACTGGTAAAC | CAACACATTC | TGAAGGATAC | ATTACTTAGT | GATAGATTCT | 360 |
| TATGTACTTT | GCTANATNAC | GTGGATATGA | GTTGACAAGT | TTCTCTTTCT | TCAATCTTTT | 420 |
| AAGGGGCNGA | NGAAATGAGG | AAGAAAAGAA | AAGGATTACG | CATACTGTTC | TTTCTATNGG | 480 |
| AAGGATTAGA | TATGTTTCCT | TTGCCAATAT | TAAAAAATA | ATAATGTTTA | CTACTAGTGA | 540 |
| AACCC | | | | | | 545 |

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTTTTTTTTT | TTTTTAGTC | AAGTTTCTNA | TTTTTATTAT | AATTAAAGTC | TTGGTCATTT | 60 |
| CATTIATTAG | CTCTGCAACT | TACATATTTA | AATTAAAGAA | ACGTTNNTAG | ACAACTGTNA | 120 |
| CAATTTATAA | ATGTAAGGTG | CCATTATTGA | GTANATATAT | TCCTCCAAGA | GTGGATGTGT | 180 |
| CCCTTCTCCC | ACCAACTAAT | GAANCAGCAA | CATTAGTTTA | ATTTTATTAG | TAGATNATAC | 240 |
| ACTGCTGCAA | ACGCTAATTC | TCTTCTCCAT | CCCCATGTNG | ATATTGTGTA | TATGTGTGAG | 300 |
| TTGGTNAGAA | TGCATCANCA | ATCTNACAAT | CAACAGCAAG | ATGAAGCTAG | GCNTGGGCTT | 360 |
| TCGGTGAAAA | TAGACTGTGT | CTGTCTGAAT | CAAATGATCT | GACCTATCCT | CGGTGGCAAG | 420 |
| AACTCTTCGA | ACCGCTTCCT | CAAAGGCNGC | TGCCACATTT | GTGGCNTCTN | TTGCACTTGT | 480 |
| TTCAAAA | | | | | | 487 |

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TGAATTGGCT | AAAAGACTGC | ATTTTTANAA | CTAGCAACTC | TTATTCTTT | CCTTTAAAAA | 60 |
| TACATAGCAT | TAAATCCCAA | ATCCTATTTA | AAGACCTGAC | AGCTTGAGAA | GGTCACTACT | 120 |
| GCATTTATAG | GACCTTCTGG | TGGTTCTGCT | GTTACNNTTG | AANTCTGACA | ATCCTTGANA | 180 |
| ATCTTTGCAT | GCAGAGGAGG | TAAAAGGTAT | TGGATTTTCA | CAGAGGAANA | ACACAGCGCA | 240 |
| GAAATGAAGG | GGCCAGGCTT | ACTGAGCTTG | TCCACTGGAG | GGCTCATGGG | TGGGACATGG | 300 |
| AAAAGAAGGC | AGCCTAGGCC | CTGGGGAGCC | CA | | | 332 |

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| AGGGCGTGGT | GCGGAGGGCG | TTACTGTTTT | GTCTCAGTAA | CAATAAATAC | AAAAAGACTG | 60 |
| GTTGTGTTC | GGCCCCATCC | AACCACGAAG | TTGATTCTC | TTGTGTGCAG | AGTGACTGAT | 120 |
| TTTAAAGGAC | ATGGAGCTTG | TCACAATGTC | ACAATGTCAC | AGTGTGAAGG | GCACACTCAC | 180 |
| TCCCGCGTGA | TTACATTTA | GCAACCAACA | ATAGCTCATG | AGTCCATACT | TGTAAATACT | 240 |
| TTTGGCAGAA | TACTTNTTGA | AACTTGCAGA | TGATAACTAA | GATCCAAGAT | ATTTCCCAAA | 300 |
| GTAAATAGAA | GTGGGTCATA | ATATTAATTA | CCTGTTTACA | TCAGCTTCCA | TTTACAAGTC | 360 |
| ATGAGCCAG | ACACTGACAT | CAAACCTAAGC | CCACTTAGAC | TCCTCACCAC | CAGTCTGTCC | 420 |
| TGTCATCAGA | CAGGAGGCTG | TCACCTTGAC | CAAATTCTCA | CCAGTCAATC | ATCTATCCAA | 480 |
| AAACCATTAC | CTGATCCACT | TCCGTAATG | CACCACCTTG | GTGA | | 524 |

(2) INFORMATION FOR SEQ ID NO:209:

120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

| | |
|---|-----|
| GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATCCAGT GTCAGCATTC TTGCTCCTTG | 60 |
| TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA | 120 |
| CAAAGGACTC TCGACCCAAA CTGCCCCAGA CCCTCTCCA | 159 |

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

| | |
|---|-----|
| ACTCCCTGGC AGACAAAGGC AGAGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAACTGCC | 60 |
| ACTGAATTTT TTTCCACTTG GACTATTACA TGCCANTTGA GGGACTAATG GAAAAACGTA | 120 |
| TGGGGAGATT TTANCCAATT TANGTNTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT | 180 |
| TTGCAGGGTG NAAATGGGAN GGCTGGTTTG TTANATGAAC AGGGACATAG GAGGTAGGCA | 240 |
| CCAGGATGCT AAATCA | 256 |

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

| | |
|---|-----|
| ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG | 60 |
| ACTGGAACAC ATACCCACAT CTTTGTCTTG AGGGATAATT TTCTGATAAA GTCTTGCTGT | 120 |
| ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTTAAGGAGA | 180 |
| GGGGAGATAC ATTCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAGA | 240 |
| AAAAAAGGAG CAAATGAGAA GCCT | 264 |

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

121

| | |
|---|-----|
| ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTTT GATTGTCAAA | 60 |
| GGATTTAATG TTGTCTCAGC TTGGGCACTT CAGTTAGGAC CTAAGGATGC CAGCCGGCAG | 120 |
| GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAACT TGCCCGCCAG | 180 |
| TTNAATTTCA TTCCCATGGA CTTGGGATCC TTATCATCAG CCAGAGAGAT TGAAAATTTA | 240 |
| CCCCTACNAC TCTTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACA | 300 |
| TTTTTTTTTC CTTTATTCCT TTGTCAGA | 328 |

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

| | |
|---|-----|
| ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AACTGAATT CTCTCCAGTT | 60 |
| TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT | 120 |
| CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT | 180 |
| TTCAATATTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT | 240 |
| TCTCATCGGT | 250 |

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

| | |
|--|-----|
| ACCCAGAATC CAATGCTGAA TATTTGGCTT CATTATTCCC AGATTCTTTG ATTGTCAAAG | 60 |
| GATTTAATGT TGTCTCAGCT TGGGCACTTC AGTTAGGACC TAAGGATGCC AGCCGGCAGG | 120 |
| TTTATATATG CAGCAACAAT ATTCAAGCGC GACAACAGGT TATTGAACTT GCCCGCCAGT | 180 |
| TGAATTTTAT TCCCATGAC TTGGGATCCT TATCATCAGC CANAGAGATT GAAAATTTAC | 240 |
| CCCTACGACT CTTTACTCTC TGGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT | 300 |
| TTTTTTTTCC TTTATTCCTT TGTCAGAGAT GCGATTTCATC CATATGCTAN AAACCAACAG | 360 |
| AGTGACTTTT ACAAATTCCT TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT | 420 |
| ACTTTGCTCT CCCTAATATA CCTC | 444 |

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

| | |
|---|-----|
| ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AACTGAATT CTCTCCAGTT | 60 |
| TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT | 120 |

122

| | |
|---|-----|
| CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT | 180 |
| TTCAATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT | 240 |
| TCTCATCGGT AAGCAGAGGC TGTAGGCAAC ATGGACCATA GCGAANAAAA AACTTAGTAA | 300 |
| TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCAA GGTGGAATC TCCTATACTT | 360 |
| GGTGCC | 366 |

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

| | |
|---|-----|
| CTGTATAAAC AGAACTCCAC TGCANGAGGG AGGGCCGGGC CAGGAGAATC TCCGCTTGTC | 60 |
| CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNTAA GGGCTNTNC ATTTTTTTAT | 120 |
| TAATAAAAAG TNNAAGGC CTCTTCTCAA CTTTTTCCC TTNGGCTGGA AAATTTAAAA | 180 |
| ATCAAAAATT TCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT | 240 |
| AATTCTTCCT TCCCTCCTTT | 260 |

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

| | |
|--|-----|
| ACCTACGTGG GTAAGTTTAN AAATGTTATA ATTTTCAGGAA NAGGAACGCA TATAATTGTA | 60 |
| TCTTGCTTAT AATTTTCTAT TTTAATAAGG AAATAGCAAA TTGGGGTGGG GGGAATGTAG | 120 |
| GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTTT | 180 |
| ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATT ATAATTAGCC ACTTACCCTA | 240 |
| ATATCCTTCA TGCTTGTAAG GT | 262 |

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

| | |
|---|-----|
| ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCCAA CCCCTGAGCA | 60 |
| CCCCTATCAA CTCCCTTTTG TAGTAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC | 120 |
| AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGTNTNA NGTCCAGGGT TGCTAGGAAA | 180 |
| ANAAATCAGC AGACACAGGT GTAAA | 205 |

(2) INFORMATION FOR SEQ ID NO:219:

123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

| | |
|---|-----|
| TACTGTTTTG TCTCAGTAAC AATAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA | 60 |
| ACCACGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TTAAAGGACA TGGA | 114 |

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

| | |
|---|----|
| ACTAGCCAGC ACAAAGGCA GGGTAGCCTG AATTGCTTTC TGCTCTTAC ATTTCTTTTA | 60 |
| AAATAAGCAT TTAGTGCTCA GTCCTACTG AGT | 93 |

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

| | |
|---|-----|
| ACTANGTGCA GGTGCGCACA AATATTGTC GATATTCCT TCATCTTGGA TTCCATGAGG | 60 |
| TCTTTTGCCC AGCCTGTGGC TCTACTGTAG TAAGTTTCTG CTGATGAGGA GCCAGNATGC | 120 |
| CCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCCAA CCTCTGT | 167 |

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

| | |
|---|-----|
| AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCCC | 60 |
| GTCTTTCACC TGTCCTCCAA TCCTTAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA | 120 |
| ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAATAA TGAATTTTGG CATAATCCAA | 180 |
| TTTTCTCTTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGGAACTCTT | 240 |
| TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTTACA TATATCTGGC ATATTGAGT | 300 |

CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T

351

(2) INFORMATION FOR SEQ ID NO:223

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

| | |
|--|-----|
| AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAGAAAA ATTATCTTAG GGACTGATAT | 60 |
| TGGTAATTAT GGTCAATTTA ATWRTRTTKT GGGGCATTTT CTTACATTGT CTTGACAAGA | 120 |
| TTAAATGTC TGTGCCAAAA TTTTGTATTT TATTTGGAGA CTTCTTATCA AAAGTAATGC | 180 |
| TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTTGGAG TGTGCTATTC | 240 |
| TAAAAGATTT TGATTTCTCTG GAATGACAAT TATATTTTAA CTTTGGTGGG GGAAANAGTT | 300 |
| ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGTC ACTTGTTTTG | 360 |
| ACCATTAAGC TATATGTTTA AAA | 383 |

(2) INFORMATION FOR SEQ ID NO:224

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 320 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

| | |
|---|-----|
| CCCCGAAGG CTTCTTGTTA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA | 60 |
| AAAAGTTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAT | 120 |
| GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTATCAT ATGTTCTAAA AGAGAAGGAA | 180 |
| GAGAAAATAC TACTTTCTCR AAATGGAAGC CCTTAAAGGT GCTTTGATAC TGAAGGACAC | 240 |
| AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT | 300 |
| TTTARACTCM GCATTGTGAC | 320 |

CLAIMS

1. A polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.
2. A DNA molecule comprising a nucleotide sequence encoding the polypeptide of claim 1.
3. A DNA molecule having a sequence provided in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224.
4. An expression vector comprising the DNA molecule of claims 2 or 3.
5. A host cell transformed with the expression vector of claim 4.
6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cell lines.
7. A pharmaceutical composition comprising the polypeptide of claim 1 and a physiologically acceptable carrier.
8. A vaccine comprising the polypeptide of claim 1 and a non-specific immune response enhancer.

9. The vaccine of claim 8 wherein the non-specific immune response enhancer is an adjuvant.

10. A vaccine comprising the DNA molecule of claims 2 or 3 and a non-specific immune response enhancer.

11. The vaccine of claim 10 wherein the non-specific immune response enhancer is an adjuvant.

12. A pharmaceutical composition for the treatment of prostate cancer comprising a polypeptide and a physiologically acceptable carrier, the polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

13. A vaccine for the treatment of prostate cancer comprising a polypeptide and a non-specific immune response enhancer, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences

14. The vaccine of claim 13 wherein the non-specific immune response enhancer is an adjuvant.

15. A vaccine for the treatment of prostate cancer comprising a DNA molecule and a non-specific immune response enhancer, the DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

16. The vaccine of claim 15 wherein the non-specific immune response enhancer is an adjuvant.

17. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claims 7 or 12.

18. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of any one of claims 8, 10, 13 or 15.

19. A fusion protein comprising two or more polypeptides according to claim 1.

20. A fusion protein comprising a polypeptide according to claim 1 and a known prostate antigen.

21. A pharmaceutical composition comprising a fusion protein according to any one of claims 19-20 and a physiologically acceptable carrier.

22. A vaccine comprising a fusion protein according to any one of claims 19-20 and a non-specific immune response enhancer.

23. The vaccine of claim 22 wherein the non-specific immune response enhancer is an adjuvant.

24. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claim 21.

25. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of claim 22.



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

| | | | | | | | | | | | |
|--|-----------------------------|--|-----------------------------|----|------------|--------------------------|----|------------|----------------------------|----|--|
| (51) International Patent Classification 6 : C12N 15/12, C07K 14/705, C12N 5/10, 1/21, A61K 38/17, C12N 1/19, A61K 39/00, C12N 15/62 | A3 | (11) International Publication Number: WO 98/37093 (43) International Publication Date: 27 August 1998 (27.08.98) | | | | | | | | | |
| (21) International Application Number: PCT/US98/03492 (22) International Filing Date: 25 February 1998 (25.02.98) (30) Priority Data: <table border="0" style="width: 100%;"><tr><td style="width: 30%;">08/806,099</td><td style="width: 30%;">25 February 1997 (25.02.97)</td><td style="width: 40%;">US</td></tr><tr><td>08/904,804</td><td>1 August 1997 (01.08.97)</td><td>US</td></tr><tr><td>09/020,956</td><td>9 February 1998 (09.02.98)</td><td>US</td></tr></table> (71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US). (72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US). (74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US). | | 08/806,099 | 25 February 1997 (25.02.97) | US | 08/904,804 | 1 August 1997 (01.08.97) | US | 09/020,956 | 9 February 1998 (09.02.98) | US | (81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 17 December 1998 (17.12.98) |
| 08/806,099 | 25 February 1997 (25.02.97) | US | | | | | | | | | |
| 08/904,804 | 1 August 1997 (01.08.97) | US | | | | | | | | | |
| 09/020,956 | 9 February 1998 (09.02.98) | US | | | | | | | | | |
| (54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE (57) Abstract Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides. | | | | | | | | | | | |

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| DK | Denmark | LR | Liberia | SE | Sweden | | |
| EE | Estonia | | | SG | Singapore | | |

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/03492

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C07K14/705 C12N5/10 C12N1/21 A61K38/17
C12N1/19 A61K39/00 C12N15/62

According to International Patent Classification (IPC) or to both national classification and IPO

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|---|-----------------------|
| A | WO 95 04548 A (JENNER TECHNOLOGIES) 16 February 1995 see the whole document --- | |
| A | WO 93 25224 A (VETROGEN CORP) 23 December 1993 see the whole document --- | |
| A | WO 95 30758 A (MAYO FOUNDATION ;HYBRITECH INC (US); TINDALL DONALD J (US); YOUNG) 16 November 1995 see the whole document --- | |
| A | EP 0 652 014 A (NAT INST IMMUNOLOGY) 10 May 1995 see the whole document --- | |
| | -/-- | |

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

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- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *Z* document member of the same patent family

Date of the actual completion of the international search

30 July 1998

Date of mailing of the international search report

03.11.1998

Name and mailing address of the ISA

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Fax: (+31-70) 340-3016

Authorized officer

Oderwald, H

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/03492

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|-----------------------|
| X | <p>SHORT J M ET AL: "LAMBDA ZAP: A BACTERIOPHAGE LAMBDA EXPRESSION VECTOR WITH IN VIVO EXCISION PROPERTIES" NUCLEIC ACIDS RESEARCH, vol. 16, no. 15, 1988, pages 7583-7600, XP002007597 see the whole document & "AC No. AA453562" EMBL SEQUENCE DATABASE, 10 May 1990, HEIDELBERG, GERMANY, see nucleotides 398-765 ---</p> | 2,4-6 |
| X,P | <p>HILLIER L ET AL: "Homo sapiens cDNA clone 788180 (AC No. AA453562)" EMBL SEQUENCE DATABASE, 11 June 1997, HEIDELBERG, GERMANY, XP002073072 see the whole document -----</p> | 2,4-6 |

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/03492

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 17, 18, 24 and 25 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see further information sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see further information sheet, subject 1.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-11 and 17-25 all partially

A polypeptide comprising an immunogenic portion or a variant of a prostate protein encoded by SEQ ID NO:2, DNA molecules related to said protein, expression vectors comprising said DNA molecules, hosts transformed with said vectors, fusion proteins comprising said polypeptide, pharmaceutical compositions and vaccines comprising said polypeptide, fusion proteins and DNA.

2. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 3.

3. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 8.

4. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 9.

5. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 10.

6. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 11.

7. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 12.

8. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 13.

9. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 14.

10. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 15.

11. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 16.

12. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 17.

13. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 18.

14. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 19.

15. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 20.

16. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 21.

17. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 22.

18. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 23.

19. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 24.

20. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 25.

21. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 26.

22. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 27.

23. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 28.

24. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 29.

25. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 41.

26. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 42.

27. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 43.

28. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 44.

29. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 45.

30. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 47.

31. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 48.

32. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210.

same as invention 1 but for SEQ ID NO: 49.

33. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 50.

34. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 51.

35. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 52.

36. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 54.

37. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 55.

38. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 56.

39. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 57.

40. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 58.

41. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 59.

42. Claims: 1-11 and 17-25 all partially
same as invention 1 but for SEQ ID NO: 60.

43. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 61.

44. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 62.

45. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 63.

46. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 64.

47. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 65.

48. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 70.

49. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 73.

50. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 74.

51. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 79.

52. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 81.

53. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 87.

54. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 90.

55. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 92.

56. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 93.

57. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 97.

58. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 103.

59. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 104.

60. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 107.

61. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 109.

62. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 110.

63. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 111.

64. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 115.

65. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 116.

66. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 117.

67. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 118.

68. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 119.

69. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 120.

70. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 121.

71. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 122.

72. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 123.

73. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 124.

74. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 125.

75. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 126.

76. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 127.

77. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 128.

78. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 129.

79. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 130.

80. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 131.

81. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 132.

82. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 133.

83. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 134.

84. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 135.

85. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 136.

86. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 137.

87. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 138.

88. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 139.

89. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 140.

90. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 141.

91. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 142.

92. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 143.

93. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 144.

94. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 145.

95. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 146.

96. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 147.

97. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 148.

98. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 149.

99. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 150.

100. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 151.

101. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 152

102. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 153.

103. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 154.

104. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 155.

105. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 156.

106. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 157.

107. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 158.

108. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 159.

109. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 160.

110. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 171.

111. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 173.

112. Claims: 1-11 and 17-25

same as invention 1 but for SEQ ID NO: 174.

113. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 175.

114. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 177.

115. Claims: 1-11 and 17-25

same as invention 1 but for SEQ ID NO: 181.

116. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 188.

117. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 191.

118. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 193.

119. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 194.

120. Claims: 1-11 and 17-25 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

same as invention 1 but for SEQ ID NO: 198.

121. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 203.

122. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 204.

123. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 207.

124. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 209.

125. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 210.

126. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 211.

127. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 220.

128. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 222.

129. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 223.

130. Claims: 1-11 and 17-25 all partially

same as invention 1 but for SEQ ID NO: 224.

131. Claims: 12-18 all partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Pharmaceutical compositions and a vaccines comprising an immunogenic portion or a variant of a prostate-specific polypeptide and related DNA sequences, said DNA sequences recited in SEQ ID NO: 5.

132. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 6.

133. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 7.

134. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 30.

135. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 31.

136. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 32.

137. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 33.

138. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 34.

139. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 35.

140. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 36.

141. Claims: 12-18 all partially

same as invention 131 but for SEQ ID NO: 37.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

142. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 38.
143. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 39.
144. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 40.
145. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 46.
146. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 53.
147. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 66.
148. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 67.
149. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 68.
150. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 69.
151. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 71.
152. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 72.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

153. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 75.
154. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 76.
155. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 77.
156. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 78.
157. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 80.
158. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 82.
159. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 83.
160. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 84.
161. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 85.
162. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 86.
163. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 88.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

164. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 89.
165. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 91.
166. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 94.
167. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 95.
168. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 96.
169. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 98.
170. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 99.
171. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 100.
172. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 101.
173. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 102.
174. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 105.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

175. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 106.
176. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 161.
177. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 162.
178. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 163.
179. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 164.
180. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 165.
181. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 166.
182. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 167.
183. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 168.
184. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 169.
185. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 170.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

186. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 179.
187. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 180.
188. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 182.
189. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 183.
190. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 184.
191. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 185.
192. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 186.
193. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 187.
194. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 189.
195. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 190.
196. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 192.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

197. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 195.
198. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 196.
199. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 197.
200. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 199.
201. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 200.
202. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 201.
203. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 202.
204. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 205.
205. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 206.
206. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 208.
207. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 212.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

208. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 213.
209. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 214.
210. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 215.
211. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 216.
212. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 217.
213. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 218.
214. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 219.
215. Claims: 12-18 all partially
same as invention 131 but for SEQ ID NO: 221.

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